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Reed SG, Lodes MJ, Mohamath R, Secrist H, Benson DR, Indirias CY;
Henderson RA, Fling SP, Algate PA, Elliot M, Mannion J, Kalos MD;
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Mouse 5HT receptor
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Homo sapiens gluco
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Human polypeptide
Human colon cancer
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Human polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                   (without alignments)
239.005 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | STDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| STDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| STDS2/gcgdata/geneseq-embl/AA1981.DAT:*
| STDS2/gcgdata/geneseq-geneseqp-embl/AA1981.DAT:*
| STDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
| STDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
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| STDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
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| STDS2/gcgdata/geneseqfyeneseqp-embl/AA1987.DAT:*
| STDS2/gcgdata/geneseqg-embl/AA1988.DAT:*
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                                                                                                                                                                                                                                                                                           -- EVEVSRDHASLGDSETLSQT......LTGGCLPWATRSHLGRRKCS 97
                                                                                                                                        July 9, 2003, 15:05:28 ; Search time 54.0796 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                908470 seqs, 133250620 residues
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AAE03740
AAE20598
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AAO13020
AAO04640
AAO09875
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ABB17957
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maximum Match 100%
Listing first 45 summaries
                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A_Geneseq_101002:*
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Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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Maximum Match 100
                                                                                                                                                                                                                                                               US-09-854-133-586
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163
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423
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68
68
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                                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
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8
                                                                                                                                                                                   Run on:
                                                                                                                                                                                                                                                                                     Title:
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Arabidopsis thalia
Arabidopsis thalia
Human G-Protein Co
Arabidopsis thalia
Arabidopsis thalia
                                                                            Human polypeptide
Human polypeptide
Plasmodium falcipa
Novel human diagno
Novel human diagno
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Arabidopsis thalia
Serotonin 5HTlc re
                                                                                                                                                                                                                                    Murine protein 1so
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                                                                                                                                                                                                                     Drosophila melanog
                                                                                                                                                                                                                             Human immune/haema
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Invertebrate octop
                                                                                                                                                             D. melanogaster oc
Drosophila melanog
                                                                                                                                                                             Drosophila melanog
                                                                                                                              form of hum
                                                                                                                                                      Drosophila melanog
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                                                     Human 5-HT2C serot
Human G protein-co
                                                                      Human reproductive
                               Human ORFX protein
Human secreted pro
        Human mutant G pro
               Human serotonin re
                        protein sequ
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Active form of hum
                                                                                                                                                                                                              Vicia sativa
                                                                                                                         Common bean
                                                                                                                                                                                                                                                                                                                                                                                            Human T cell epitope related to lung tumour-specific protein.
                                                                                                                               Active
                           Human
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                                                                                                                                                                                                                                                           AAG47016
AAU27511
                                                                                                                                                                                                                            ABB60070
AAM86657
                                                                                                                                                                                                                                            ABB72349
AAG47017
                                                                                                                                                                                                            AAP90549
                                                                                                                                                                                                                     AAY05896
                                                                                                                                                                     AAY33680
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                                                                                                                                                                            AAY25464
                                                                                                                                                                                    ABB65092
             AAY90676
AAB45803
                                                                                                             ABG26719
                                                                                                                     ABG11242
                                                                                                                               AAM51135
                                                                                                                                    AAY 28853
                                                                      AAY90641
                                                                                     AA012091
                                                                                                      AAB1835
      AAY28851
                                                                                                                                                                                                                                                                                                                                                  AAE13851 standard; peptide; 16 AA.
                                                                                                                                                                                             AAU45
AAG07
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18-AUG-2000; 2000US-0640818.
22-SEP-2000; 2000US-234517P.
01-NOV-2000; 2000US-0704512.
14-DEC-2000; 2000US-0738973.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-MAR-2000; 2000US-0538037.
05-JUN-2000; 2000US-0588937.
18-AUG-2000; 2000US-0640878.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-MAR-2001; 2001WO-US09991.
        26-FEB-2002 (first entry)
        458
458
105
105
1190
458
458
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2138
2197
2100
3697
637
637
642
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637
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                                                                                                                                                                                                                                                                                                                                                                                                                                      cell epitope.
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                                                                                   The invention relates to isolated lung tumour-specific proteins and their corresponding cDNA molecules. Lung tumour-specific proteins and their antigen-presenting cells are useful for stimulating and/or the development of cancer. The invention protein, and for inhibiting lung the development of cancer. The invention also relates to a composition lung tumour specific oil immune response, and for treating cancer. The lung tumour specific oilgonucleotide is useful in gene therapy and for diagnosis, detection and treatment of lung cancer. The present sequence is human T cell epitope related to lung tumour-specific protein.
                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or
                                                                                                                                                                                                                                                           Gaps
                              New human lung-specific polynuclectides and polypeptides for the diagnosis and treatment of disease e.g. lung cancer -
                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; SEQ ID NO 26912; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                   Length 16;
                                                                                                                                                                                                                       18.4%; Score 98; DB 22; Length 16
100.0%; Pred. No. 0.0002;
Live 0; Mismatches 0; Indels
                                                              Claim 2; Page 378; 378pp; English.
                                                                                                                                                                                                                                                                                                                                      AA013020 standard; Protein; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                      Human polypeptide SEQ ID NO 26912.
                                                                                                                                                                                                                                                             35 FOANCGIDFIIFWIFW 50
                                                                                                                                                                                                                                                                             1 FOANCGIDFILFWIFW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                               06-NOV-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-MAY-2000; 2000US-0577409
                                                                                                                                                                                                                                             Conservative
          WPI; 2001-639201/73.
                                                                                                                                                                                                                                Local Similarity
es 16; Conserv
                                                                                                                                                                                                 16 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                            AA013020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorders
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                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                 RESULT 2
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Peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activinhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                   10 SLGDSETLSQTEL---RKKERKKKRERKFQANCG-IDFIIFWIFWILLFSHHWIQESLLC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
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                                                                                                                                                                                                                                                                                                                       15.4%; Score 82; DB 22; Length 121;
34.1%; Pred. No. 0.13;
tive 4; Mismatches 20; Indels 30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acids and polypeptides, useful for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID NO 18532; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                         at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                        Local Similarity 34.1%; Pred. No. 0.13 es 28; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 -----TCNH-----LPWLT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 PPSPKEVTCREMLTGGCLPWAT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA004640 standard; Protein; 46 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-2001; 2001WO-US04927.
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                                                                                                                                                                                                                                                                    121 AA;
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                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                 Matches
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8 x c c c c c c

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemla; nervous system disorders; arthritis; inflammation.
                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID NO 23767; 1399pp + Sequence Listing; English.
                                                                                                                                                                 7;
                                                                                                                                13.4%; Score 71.5; DB 22; Length 46; 81.0%; Pred. No. 0.69; 2; Indels 1tive 1; Mismatches 2; Indels 1
                                                                                                                                                                                                                                                                                                                     AA009875 standard; Protein; 141 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                  Human polypeptide SEQ ID NO 23767.
                                                                                                                                                                                                          14 SETLSQTELRKKERKKKERK 34
                                                                                                                                                                                                                         Tang YI, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                                                         06-NOV-2001 (first entry)
                                                                                                                                                          Best Local Similarity 81.0° Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 141 AA;
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                                                                                                                     46 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200164835-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                           AA009875;
                                                                                                                         Sednence
                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                 RESULT 4
AAO09875
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AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where cancer-associated nucleic acid molecules (N) and proteins. The colon the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in the prevention. Cancer antigens have cytostatic activity and can be used in the prevention, therapy and vaccine production. N and P may be used in the prevention. Captression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions associated with decreased expression by rectifying mutations or deletions cancer associated ps, additionally, N may be used to produce the colon cancer-associated Ps. Additionally, N may be used to produce the colon cancer-associated Ps. Colorecting the nucleic acids into a host cell and culturing the cell of the express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers, AAH37196 to AAH37204 and AAH37199 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                     ä
                                                                                                       1 EVEVSRD---HASLGDSETLSQTELRKKERKKRE-----RKFQANCGIDFIIFWIFWIL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention.
N.B. Pages 666 to 682 and page 7053 of the sequence listing were
N.B. Pages 610 to 682 and page 7053 of the sequences are present for
SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                         5 KVAVSYDLIMHSNLSNSETLSOKEKTKOTKTKOKKTYXEGRKHIKRCPTPLIIREIQIOT 64
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; colon cancer; colon cancer antigen; diagnosis; detection;
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                                                             6
13.4%; Score 71.5; DB 22; Length 141; 31.0%; Pred. No. 2.5;
                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human colon cancer antigen protein SEQ ID NO:6226.
                                                                   36;
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38.6%; Pred. No. 2.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Page 7674-7676; 9803pp; English.
                                                                      13; Mismatches
                                                                                                                                                                                                                                   53 LFSHHWIQ-ESLLCPPSPKEVTCR 75
                                                                                                                                                                                                                                                                                        65 TVRYHFTHIRIVLLPOKONKCWCR 88
                                                                                                                                                                                                                                                                                                                                                                                                                             AAG75462 standard; Protein; 163 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
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                                                                                  26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        colorectal carcinoma
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                                         Query Match
Best Local Similarity
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05-SEP-2000; 2000US-0239513.

06-SEP-2000; 2000US-0230437.

08-SEP-2000; 2000US-0231242.

08-SEP-2000; 2000US-0231242.

08-SEP-2000; 2000US-0231243.

08-SEP-2000; 2000US-0231244.

08-SEP-2000; 2000US-0231241.

08-SEP-2000; 2000US-0232080.

08-SEP-2000; 2000US-0232080.

08-SEP-2000; 2000US-0232080.
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2000US-0233065.
2000US-0234223.
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02-0CT-2000; 2000US-0237038
02-0CT-2000; 2000US-0237039
13-0CT-2000; 2000US-0239935
20-0CT-2000; 2000US-0239935
20-0CT-2000; 2000US-0249935
20-0CT-2000; 2000US-0241785
20-0CT-2000; 2000US-0241785
20-0CT-2000; 2000US-0241786
20-0CT-2000; 2000US-0241808
20-0CT-2000; 2000US-0241806
20-0CT-2000; 2000US-0241806
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20000S-0235834.
20000S-0235836.
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2000us-0236367.
2000us-0236368.
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2000US-0232400
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2000US-0233063
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2000US-0236370.
2000US-0236802.
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2000us-0246476
2000us-0246476
2000us-0246477
2000us-0246477
2000us-0246677
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2000US-0246526.
2000US-0246527.
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2000US-0246532.
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2000US-0249208
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14-SEP-2000;
14-SEP-2000;
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14-SEP-2000;
21-SEP-2000;
21-SEP-2000;
25-SEP-2000;
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26-SEP-2000;
27-SEP-2000;
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                                     Oytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; antioonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein;
                                 10 SLGD-SETLSOTELRKKERKKKRERKFOANCGIDFIIFWIFWILLFSHHWIQESLLC 65
                                                     21; Gaps
                                                                                                                                                                                                                                                    Human musculoskeletal system related polypeptide SEQ ID NO 1089.
                    9; Indels
            5; Mismatches
                                                                                                                                                  ABB03142 standard; Protein; 66 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAR-2000; 2000us-0186350.

16-MAR-2000; 2000us-0186350.

17-MAR-2000; 2000us-0190076.

18-APR-2000; 2000us-0190076.

19-MAY-2000; 2000us-020515.

07-JUN-2000; 2000us-020545.

28-JUN-2000; 2000us-0214886.

07-JUN-2000; 2000us-0214886.

07-JUL-2000; 2000us-0214886.
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24-FEB-2000; 2000US-0184664.
 22; Conservative
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2000US-0224519.
2000US-0225213.
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2000US-0225447.
2000US-0225757.
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2000US-0220964.
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14-AUG-2000;
14-AUG-2000;
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01-SEP-2000; 2
05-SEP-2000; 2
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Matches
                                                                                                                RESULT 6
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08-SEP-2000; 2000US-0232080
08-SEP-2000; 2000US-0232081
12-SEP-2000; 2000US-0231968
      23-JAN-2002 (first entry)
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                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                       31-JAN-2000;
                                                                                                                                                                                         16-AUG-2001.
The invention relates to novel genes (AAL34669-AAL37666) and proteins CC (ABB03087-ABB04109) associated with the musculoskeletal system useful CC (ABB03087-ABB04109) associated with the musculoskeletal system useful CC preventing, treating or ameliorating medical conditions e.g. by core in content or gene therapy. The genes are isolated from a range of human core is also factored in the specification. The nucleic acids, proteins, core is a prevention of: (a) cancer, e.g. breast and ovarian cancer and prevention of: (a) cancer, e.g. breast and ovarian cancer and prevention of: (a) cancer, e.g. breast and ovarian cancer and core rangers of the adrenal gland, bone, bone marrow, breast, core gastrointestinal tract, liver, lung, or urogenital; (b) immune cancers of sheadson's disease, allergies mellitus, crom's disease, and semania, autoimmune tharby disease, allergies mellitus, crom's disease, and ulcerative colitis; multiple sclerosis, rheumatoid arthritis and ulcerative colitis; multiple sclerosis, rheumatoid arthritis and ulcerative colitis; and (f) infectious diseases such as viral, bacterial, fungal and cancer in fertions diseases such as viral, bacterial, fungal and cancer in the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. WiPo.int/Pub/Published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                     Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.1%; Score 69.5; DB 22; Length 66; 50.0%; Pred. No. 1.8; tive 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; SEQ ID NO 1089; 781pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB17957 standard; Protein; 63 AA.
                                                                                                                                                                                                                                                                                                      Rosen CA, Barash SC, Ruben SM;
                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
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Best Local Similarity 50.09
Matches 19; Conservative
                                                                                                                                                                                                                                                          05-JAN-2001; 2001US-0259678.
                                                                                                                                                                                                                                  2000US-0251990.
                                                                                                                                           2000US-0251030.
                                                                                                                                                                            2000US-0251479.
                                                                                                                                                                                       2000US-0251856.
                                                            17-NOV-2000; 2000US-0249264.
17-NOV-2000; 2000US-0249265.
17-NOV-2000; 2000US-0249297.
17-NOV-2000; 2000US-0249297.
                                                                                                         2000US-0249300.
                                                                                                                                 000US-0250391.
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                                                 17-NOV-2000; 2000US-0249245.
                2000US-0249217
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N-PSDB; AAL34724.
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ID ABB1
XX ABB1
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Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; amimunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antimunosuppressive; antisathatitic; cancer; antirheumatic; the patotropic; cerebroprotective; antiinflammatory; antitheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiinflammatic; antidabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine.
Human nervous system related polypeptide SEQ ID NO 6614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0229344.
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14-AUG-2000; 2000US-0225447.
14-AUG-2000; 2000US-0225757.
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2000US-0225266.
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20-0cT-2000; 2000US-0241/85.
20-0cT-2000; 2000US-0241/86.
20-0cT-2000; 2000US-024186.
20-0cT-2000; 2000US-0241809.
20-0cT-2000; 2000US-0241809.
20-0cT-2000; 2000US-0241826.
10-NOV-2000; 2000US-024617.
08-NOV-2000; 2000US-0246475.
08-NOV-2000; 2000US-0246475.
08-NOV-2000; 2000US-0246476.
              14-SEF-2000; 2000US-V2250:
14-SEF-2000; 2000US-V23063:
14-SEF-2000; 2000US-0233064:
2000US-0232399
                                                                                                                     2000US-0234997
                                                                                                                                                                 2000US-0235834
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200005-0246610
200005-0246611
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21-SEP-2000;
                                                                                                                               25-SEP-2000;
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29-SEP-2000;
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29-SEP-2000;
29-SEP-2000;
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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB1678-ABB18001) useful for preventing, treating or amellorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the genesiare the interpretation of the interpretation of the dispansis, treatment and prevention of (ant)agonists are useful on the dispansis, treatment and prevention of (a) cancer, e.g. breast marrow, breast, gastrointestinal tract, liver, lung, or urogenital; chaemolytic anaemia, autoimmune thyroiditis, dispetes mellitus, crown's disease, multiple solerosis, rheumatoid arthritis and ulcerative of use and parasing (c) cardiovascular disorders such as myocardial ischaemias; epilepsy; and (f) infectious diseases e.g. cerebral anoxia and parasitic infectious diseases such as viral, bacterial, fungal Nore: The seminance data for this contains.
                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse, 5HT receptor; chimera; cDNA library preparation; serotonin; G protein-coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; SEQ ID NO 6614; 1701pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.0%; Score 69; DB 22; Length 63; 51.4%; Pred. No. 1.9; tive 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VEVSRDHASL----GDSETLSQTELRKKERKKRRE 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 VAVSQDSATTLQPGRQSKTLSQKKKKKKKKKKRE 40
                                                                                                                                                                                                                                              Rosen CA, Barash SC, Ruben SM;
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             05-DEC-2000; 2000US-025190;
05-DEC-2000; 2000US-025190;
06-DEC-2000; 2000US-0251479;
08-DEC-2000; 2000US-0251869;
08-DEC-2000; 2000US-0251869;
08-DEC-2000; 2000US-0251869;
08-DEC-2000; 2000US-0251869;
08-DEC-2000; 2000US-0251999;
                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
       2000US-0251030
                                                                                                                                                                          05-JAN-2001; 2001US-0259678;
                                                                                                                                                          11-DEC-2000; 2000US-0254097
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N-PSDB; ABA14283.
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10-JUL-2000;
11-JUL-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                   328 FAFHWFAMSSTCYNPFIYCWLNENFRVELKALLSMCORPPKPOEDRLPSPVPSFRVAWTE 387
                                                                                                                                                                                                                                                                                                                                                                Preparing a chimera cDNA library comprises recombinantly expressing cDNA with a protein translation frame and a cDNA containing a carboxy terminal side from a stored region of a functional protein synthesized
                                                                                                                                                                                                                                                                                                                          10 SLGDSETLSQTELRKKERKKKRERKFQANCGIDFIIFWI---FWILL------
                                                                                                                                                                                       The present sequence is provided in a specification relating to the preparation of a chimera cDNA library containing a cDNA encoding a functional protein. The specification describes the preparation of a serotonin-related cDNA library, and the preparation of a forcein-coupled receptor chimera cDNA library from which an orphan G protein-coupled receptor chimera spinal library from which an orphan G protein-coupled receptor cDNA was isolated.
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse; G-protein coupled receptor; GPCR; RP-23; sphingosine-1-P04; sphingosine-1-phosphate; therapy; cardiovascular disease; cancer; inflammatory disease; cell signalling.
                                                                                                                                                                                                                                                                                                       46;
                                                                                                                                                                                                                                                                                 12.8%; Score 68; DB 22; Length 423; 22.8%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                      41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse G-protein coupled receptor (GPCR) RP-23 protein.
                                                             (KUBO/) KUBO Y.
(KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN
                                                                                                                                                                                                                                                                                                     11; Mismatches
                                                (AGEN ) AGENCY OF IND SCI & TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE03740 standard; Protein; 423 AA.
                                                                                                                                                                      Example 7; Fig 6; 24pp; Japanese.
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         99JP-0373989
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                                                                                                                                                                                                                                                                                            1 Similarity 22.89 29; Conservative
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                                                                                                                                                                                                                                                               423 AA;
                                                                                                 N-PSDB; AAI69851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200144439-A2
                                                            KUBO
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        28-DEC-1999;
                            28-DEC-1999;
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Best Local
                                                           (KUBO/)
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271 TIGDVTTEQYLALR --- RKKKTTVKMLVLVVVLFALCWFPLNCYVLLLSSKAIHTNNALY 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is mouse G-protein coupled receptor (GPCR) RP-23 protein. RP-23 is a ligand for sphingosine-1-phosphate (sphingosine-1-Po4) which is formed by the breakdown of sphingolipids and is involved in cell signalling. Sphingosine-1-Po4 causes an increase in receptor-generated adenylyl cyclase activity and an increase in intracellular calcium concentration. The present invention relates to methods for determining whether a test compound modulates interactions between sphingosine-1-Po4 and RP-23 a particular G-protein coupled receptor. The method is useful for determining a modulator which binds sphingosine-1-Po4 to an RP-23 receptor. The compounds identified are useful as therapeutic agents for treating cardiovascular diseases,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Determining modulator of binding of sphingosine-1-PO4 to RP-23 receptor, involves incubating sphingosine-1-PO4 and RP-23 receptor with test compound, determining the binding and comparing with a control ^{\circ}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 SLGDSETLSQTELRKKERKKKRERKFQANCGIDFIIFWI---FWILL-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 68; DB 22; Length 423; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.8%; Score to; 22.8%; Pred. No. 22; +ive 11; Mismatches 41; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammatory diseases and cancers.
                                                                                                                                                                                                                   Disclosure; Fig 3; 25pp; English
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2000US - 217255P.
2000US - 217256P.
2000US - 217257P.
2000US - 217347P.
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2000US-217223P.
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388 KSH-GRR 393
WPI; 2001-398140/42.
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Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 423 AA;
                             N-PSDB; AAD08133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200203793-A2.
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Serotonin receptor; 5-hydroxytryptamine; human 5-HT2C; non-endogenous; active form; point mutation; third intracellular loop; specificity; linkage; transduction pathway; biological response; antagonist; AP-1; baselline intracellular response; compound; treatment; prevention; agent; central nervous system; cardiovascular disorder; drug screening; gastric or inflammatory disorder; constitutive expression.

Homo sapiens.

Active form of human 5-HT2C serotonin receptor (AP-1).

(first entry)

25-JAN-2000

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Novel non-human transgenic animal, especially transgenic mice useful for identifying an agent that modulates expression or function of target gene, comprises disruptions in target G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271 TIGDVTTEQYLALR---RKKKTTVKMLVLVVVLFALCWFPLNCYVLLLSSKAIHTNNALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.8%; Score 68; DB 23; Length 423; 22.8%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 SLGDSETLSQTELRKKERKKKRERKFQANCGIDFIIFWI---FWILL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY28851 standard; Protein; 458 AA.
                                                                                                                                                                                                                               Disclosure; Fig 7; 101pp; English.
                                                      2000US-223122P.
2000US-243958P.
2000US-249408P.
                             000US-218358P.
                                                                                 2000US-252299P.
2001US-262113P.
                   2000US-218074P
                                    2000US-221483P
                                              2000US-223120P
                                                                                                    16-JAN-2001; 2001US-262205P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29; Conservative
                                                                                                                                       Allen KD, Brennan TJ;
                                                                                                                     (DELT-) DELTAGEN INC.
                                                                                                                                                         WPI; 2002-164574/21.
N-PSDB; AAD32919.
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KSH-GRR 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RSHLGRR 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                          423 AA;
                                    27-JUL-2000;
                                                       07-AUG-2000;
                                             07-AUG-2000;
                                                                         15-NOV-2000;
                                                                                         16-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY28851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY28851
Op
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WO9952927-A1
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                                                                                                                                                                                                                                                                                                                                                                                  14-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUN-1998;
18-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAR-1999;
                                                                                                                         21-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Behan DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu Q,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a non-human transgenic animal having targetted G-protein coupled receptor (GPCR) gene disruptions in melanocottin-3 gene 5-HF-2B gene, chemoKinne receptor 9A gene, glucocorticoid-induced receptor gene, orphan GPRIS gene, orphan GPRIS gene, corphan GPRIS gene, can gene, orphan GPRIS gene, can gene, cransgenic animal is useful for identifying an agent that modulates the cappession or function of the target gene, for identifying an agent that capped construct is useful for producing a transgenic animal.

A transgenic construct is useful for producing a transgenic animal, cappersonic animal is useful for producing a transgenic animal, construct is useful for producing a transgenic animal, cappersonic mouse. The transgenic animal is useful for testing the efficacy of proposed genetic animal is useful for preferably a transgenic construct as neurological, neuropsychological or psychotic illnesses. The transgenic animal is also useful as models for diseases, disorders or conditions associated with phenotypes relating to a disruption in a target, and to identify pharmaceuticals, therapies, the the contract of the contract of the capped of the contract of the capped of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   other phenotypic characteristics of the animal. An agent which modulates the expression of the target gene is useful as a therapeutic for treating conditions associated with a disruption of the target gene. The present sequence is human glucocorticoid-induced receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FAFHWFAMSSTCYNPFIYCWLNENFRVELKALLSMCORPFKPOEDRLPSPVPSFRVAWTE 387
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RESULT 12

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         form of human 5-HT2C serotionin receptor. A point mutation replaces a Servital Library in the third intracellular loop of the 5-HT2C receptor. This activated receptor allows linkage to the transduction pathway and produces a biological response. This sequence can be used to identify antagonists that bind serotion receptors and reduces the baseline intracellular response caused by receptor activation. Constitutive expression of this receptor is suitable for drug screening and to identify agents of very high specificity. These compounds are potentially useful for treating or preventing disorders involving central nervous system and cardiovascular, gastric or inflammatory disorders, that
                                                                                                                                                                                                                                                       /note= "Ser in endogenous form of 5-HT2C replaced by Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present protein sequence is the non-endogenous, constitutively active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RDHASLGDSETLSQTELRKKERKKKR-------ERKFQANCGIDFIIFWIFWILLF 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acid, used to identify inverse agonists e.g. for treating or preventing cardiovascular disease \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liaw CW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Foster RJ, Glen RC, Lawless MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.8%; Score 68; DB 20; Length 458; 27.4%; Pred. No. 24; Live 15; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Russo JF, Smith JR, Thomsen WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          329 ITNIL--SVLC----EKSCNOKL 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 SHHWIQESLLCPPSPKEVTCREML 78
                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Fig 5b; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                         98US-0060188.
98US-0190783.
98US-0112909.
99US-0123000.
                                                                                                                                                                                                                                                                                                                                               99WO-US08168.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 27.4 Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              involves these receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AREN-) ARENA PHARM INC. (TRIP-) TRIPOS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chalmers DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-611285/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              458 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAZ08098
                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                Synthetic
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329 ITNIL--SVLC----EKSCNOKL 345

g

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The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-AAY90643-AAY90643-AAY90643-AAY90643-AAY90643-AAY90643-AAY90643-AAY90643-AAY90643-AAY90643-AAY90643-AAY90643-AAY90643-AAY90643-AAY90643-AAY90643-AAY90643-AAY90643-AAY90683-AAY90683-AAY90743-AAY90683-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90643-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY90763-AAY9077-AAY90763-AAY9077-AAY90763-AAY9077-AAY90763-AAY90763-AAY9077-AAY90763-AAY90763-AAY9077-AAY90763-AAY90763-AAY9077-AAY90763-AAY9077-AAY90763-AAY9077-AAY90763-AAY9077-AAY90763-AAY9077-AAY90763-AAY9077-AAY9077-AAY90763-AAY9077-AAY9077-AAY90763-AAY9077-AAY9077-AAY9077-AAY90763-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY9077-AAY90743-AAY90743-AAY90743-AAY907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 RDHASLGDSETLSQTELRKKERKKKR------ERKFQANCGIDFIIFWIFWILLF 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                       G protein-coupled receptor; GPCR; constitutively active; intracellular loop 3; transmembrane domain 6; drug screening; agonist; antagonist; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21; Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28; Indels
                                                                                                                                                           Human mutant G protein-coupled receptor 5HT-2C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 297-298; 341pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.8%; Score 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 SHHWIQESLLCPPSPKEVTCREML 78
                         AAY90676 standard; Protein; 458 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liaw CW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US23938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0170496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.48;
                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Behan DP, Chalmers DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AREN-) ARENA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-329165/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           458 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAA30742.
                                                                                                                                                                                                                                                                                                                                                              WO200022129-A1.
                                                                                                                 21-AUG-2000
                                                                                                                                                                                                                                                                                               sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                            20-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                     AAY90676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
AAY90676
                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
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-urea derivatives (I) which are modulators of non-endogenous, constitutively activated forms of serotonin 5-HT2A (and 5-HT2A) receptors and inverse agonists to 5-HT2A receptors. (I) modulate serotonin 5-HT(2A) receptor activity and are potentially useful for treating central nervous system (CNS), gastrointestinal, cardiovascular and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes novel 1-Phenyl-3-(3-(4-bromo-3-pyrazoly1)phenyl)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New 1-phenyl-3-(3-(4-bromo-3-pyrazolyl)phenyl)-urea derivatives, useful as 5-HT(2A) receptor ligands e.g. for treating central nervous system, gastrointestinal, cardiovascular and inflammatory disorders
                                                                                                                                                                                                                                                                                                            1-Phenyl-3-(3-(4-bromo-3-pyrazolyl)phenyl)-urea derivative; modulator; central nervous system disorder; CNS; gastrointestinal disorder; cardiovascular disorder; inflammatory disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 RDHASLGDSETLSQTELRKKERKKKR------ERKFQANCGIDFIIFWIFWILLF
                                                                                                                                                                                                                                                                                  Human serotonin receptor; 5-HT2A receptor; 5-HT2C receptor; agonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Menzaghi F, Russo JF;
, Liaw CW, Beeley NRA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22; Length 458;
                                                                                                                                                                                                                       Human serotonin receptor associated protein SEQ ID NO 23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chalmers DT, Behan DP, Liu Q, M
Thomsen WJ, Glen RC, Lawless MS,
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                             AAB45803 standard; Protein; 458 AA.
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99US-0292069.
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Matches 23; Conserv
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Smith JR,
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AAB45803
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The present invention describes primer sets for synthesising 5602

full-length cDNAs defined in the specification. Where a primer set

comprises: (a) an oligo-dr primer and an oligonucleotide comprises one of

the 5602 nucleotide sequences defined in the specification, where the

oligonucleotide comprises at least 15 nucleotides; or (b) a combination

of an oligonucleotide comprising a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end

sequence and an oligonucleotide comprising a sequence complementary to a

complementary strand of a polynucleotide which comprises a 5'-end

complementary strand of a polynucleotide which comprises a 5'-end

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complementary strand of a polynucleotide on the complementary to a

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the 5602 nucleotide which comprises at least 15 nucleotides and the complementary to the

complementary strand of the primers are useful for synthesisting polynucleotides,

the 5'-end sequence/3'-end sequence is selected from those defined in

the specification. The primers are useful for synthesisting polynucleotides,

the full-length cDNAs. The primers are also useful for the

detection and/or diagnosis of the abnormality of the proteins encoded by

the full-length cDNAs. The primers allow obtaining of the full-length

CONAs easily without any specialised methods. AAH(3618 to AAH(3629 to AAH(3632)

AAH(3633 to AAH(3612 represent human anino acid sequences; and AAH(3629 to AAH(362)

of the process to oligonal eactines and one acid in the exemplification

of the process to oligonal eactines.

The process to oligonal eactines are also used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                             Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saito K, Ya
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; SEQ ID 13140; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nishikawa T, Hayashi K, S:
T, Wakamatsu A, Nagai K,
                                                                                                                 Human protein sequence SEQ ID NO:13140,
                                                                                                                                                                                                                                                                                                                                                                                             99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-318749/34.
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09-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JAN-2000;
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                     AAB93643
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Yamamoto J;

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12.7%; Score 67.5; DB 22; Length 105; ilarity 41.7%; Pred. No. 5.1; Conservative 9; Mismatches 7; Indels 5
                  Local Similarity
es 15; Conserv
Query Match
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3 EVSRDHASLGDSETLSQTELRKKERKKKRERKFQAN 38
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Matches

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Gaps

5

RESULT 15 ABP00516

Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psorthasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis; Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders Human ORFX protein sequence SEQ ID NO:1014. ABP00516 standard; Protein; 81 AA. 29-MAY-2001; 2001WO-US10836. 30-MAY-2000; 2000US-206132P. 29-AUG-2000; 2000US-228716P. (first entry) (CURA-) CURAGEN CORP. WPI; 2002-106308/14. Shimkets RA, Leach myasthenia gravis. N-PSDB; ABN16268 WO200192523-A2. Homo sapiens. 06-DEC-2001. 24 - JUN - 2002

The present interface as open reading frame, ORFX, where X is 1-11491 (see Table In the specification). ABN15762 to ABN27252 encode the human ORFX proteins are useful for proteins given in ABP00101 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide considered and in gene therapy. ORFX sequences can be used in from the protein of a sequences can be used in gene therapy. ORFX sequences can be used in the manufacture disorders, ritrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus exythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious disease, autoimmune thyroiditis, myssthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, inclsions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut proteins are also bone degenerative disorders, or periodontal disease, and for gut proteins in various tissues and conditions resulting from reperfusion injury in various tissues and conditions resulting from N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO present invention describes substantially purified human proteins ftp.wipo.int/pub/published_pct_sequences systemic cytokine damage.

Disclosure; SEQ ID 1014; 1037pp; English

Score 67; DB 23; Length 81; Pred. No. 4.3; Indels 12; 3; Mismatches 12.6%; Conservative Local Similarity les 14; Conserv 81 AA; Sequence Query Match Matches

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Gaps

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18 SQTELRKRERKKRERKFQANCGIDFIIF 46 | :|||| :||||| : | |||| ||||| 11 SHRQLRKKAKKKREARINTECVFIFFIF 39

Search completed: July 9, 2003, 15:07:40 Job time: 56.0796 secs qq

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1 EVEVSRDHASLGDSETLSQT......LTGGCLPWATRSHLGRRKCS
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-292-063-29
US-08-310-271-2
US-09-292-071-27
US-09-292-069A-27
US-09-767-013-27
US-09-292-069A-33
US-09-292-069A-33
US-09-292-069A-33
US-09-134-001C-3830
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Listing first 45 summaries
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Sequence 29, Application US/09292071
Fatent No. 6107324
GENERAL INFORMATION:
APPLICANT: Behan, Dominic
APPLICANT: Chalmers, Derick
TITLE OF INVENTION: No. 6107324-Endogenous, Constitutively Activated
TITLE OF INVENTION: Human Serotonin Receptors and Small Molecule Modulators Tivumber OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/292,071
       US-09-092-636-9

US-09-032-742-20

US-08-031-738-11

US-08-031-538-11

US-08-031-538-12

US-08-661-739-2

US-09-514-247A-18

US-09-514-247A-18

US-09-714-247A-19

US-09-714-247A-19

US-09-714-247A-19

US-08-118-270-71

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US-08-118-270-31
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US-08-767-993-11
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                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MARK J. ROSEN
RECISTRATION NUMBER: 39,822
RECISTRATION NUMBER: 39,822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 564-6525
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: April 14, 1999
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TOPOLOGY: not relevar MOLECULE TYPE: protein
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55 SHHWIQESLLCPPSPKEVTCREML 78

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Sequence

US-09-328-314-16 US-09-450-790A-2 US-09-332-837-2 PCT-US93-10553-2

Sequence

Sequence Sequence

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SEQUENCE CHARACTERISTICS: LENGTH: 458 amino acids
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    internal
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MOLECULE TYPE: protein
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TOPOLOGY: linear
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           LENGIH: 458
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APPLICANT: Russo, Joseph F
APPLICANT: Smith, Julian R
APPLICANT: Smith, Julian R
APPLICANT: Thomsen, William R
TITLE OF INVENTION: No. 6140509-Endogenous, Constitutively Activated Human
TITLE OF INVENTION: Serotconin Receptors And Small Molecule Modulators
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
FILE REFERENCE: ARBNO33
CURRENT APPLICATION NUMBER: 05/090,783
PRIOR APPLICATION NUMBER: 60/090,783
PRIOR APPLICATION NUMBER: 60/112,909
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1999-03-05
NUMBER OF SEQ ID NOS: 33
SOFFWARE: Patentin Ver. 2.1
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APPLICANT: Chalmers, Derick
TITLE OF INVENTION: No. 6420541-Endogenous, Constitutively Activated Human
TITLE OF INVENTION: Serotonin Receptors and Small Molecule Modulators
TITLE OF INVENTION: Thereo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: No. 6140509e1; OTHER INFORMATION: Sequence
US-09-292-069A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.8%; Score 68; DB 4; Length 458; 27.4%; Pred. No. 5.5; tive 15; Mismatches 28; Indels
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CURRENT APPLICATION NUMBER: US/09/767,013
CURRENT FILING DAFE: 2001-01-23
PRIOR APPLICATION NUMBER: 09/292,072
PRIOR FILING DATE: 1999-04-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 29
329 ITNIL--SVLC----EKSCNQKL 345
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                                                                                                                       Sequence 29, Application US/09292069A Patent No. 6140509
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                                                                                                                                                                                     Behan, Dominic P
Chalmers, Derek T
Foster, Richard J
Glen, Robert C
                                                                                                                                                                                                                                                                  Lawless, Michael S
Liaw, Chen W
Liu, Qian
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 12.8%
Best Local Similarity 27.4%
Matches 23; Conservative
                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                               US-09-292-069A-29
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APPLICANT:
APPLICANT:
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FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6420541el Sequence
US-09-767-013-29
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                                                                                                                                                                            28; Indels 18; Gaps
                                                                                                                         Query Match
12.8%; Score 68; DB 4; Length 458;
Best Local Similarity 27.4%; Pred. No. 5.5;
Matches 23; Conservative 15; Mismatches 28; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Lappalainen, Jaakko
APPLICANT: Linnoila, marku
APPLICANT: Linnoila, marku
APPLICANT: Goldman, David
TITLE OF INVENTION: ALLELIC VARIATION OF THE SEROTONIN
ITLE OF INVENTION: 5HT2C RECEPTOR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: NIH103.001A
ELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEPRAX: 619-235-0176
                                                                                                                                                                                                                                                                                                                                                           329 ITNIL--SVLC----EKSCNQKL 345
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/310,271
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; Patent No. 5654139
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ORGANISM: Artificial Sequence
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27.4%;
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REGISTRATION NUMBER: 36
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APPLICANT: Russo, Joseph F
APPLICANT: Smith, Julian R
APPLICANT: Smith, Julian R
APPLICANT: Thomsen, William J
TITLE OF INVENTION: No. 6140509-Endogenous, Constitutively Activated Human
TITLE OF INVENTION: Serotonin Receptors And Small Molecule Modulators
TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 RDHASLGDSETLSQTELRKKERKKKR------ERKFQANCGIDFIIFWILLF 54
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Sequence 10, Application US/09032742
Patent No. 6255089
GENERAL INFORMATION:
APPLICAMT: Teitler, Milt
APPLICAMT: Herrick-Davis, Katharine
APPLICAMT: Egan, Christina C.
TITLE OF INVENTION: Constitutively Activated Serotonin
TITLE OF INVENTION: Receptors
NUMBER OF SEQUENCES: 25
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APPLICATION NUMBER: US/09/032,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Laurence Weinberger
STREET: 882 S. Matlack Street, Suite 103
STREET: P.O. Box 1663
CITY: West Chester
                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/292,069A CURRENT FILING DATE: 1999-04-14
                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60,090,783
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/112,909
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1999-13,000
PRIOR FILING DATE: 1999-03-05
PRIOR FILING DATE: 1999-03-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 27
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                  Lawless, Michael S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Laurence
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ZIP: 19380-0053
COMPUTER READABLE FORM:
Glen, Robert C
                                        Liaw, Chen W
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US-09-032-742-10
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                                          APPLICANT:
                           APPLICANT:
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                                                                                                                                                                                                                                                                          Sequence 27, Application US/09292071
Patent No. 6107324
GENERAL INFORMATION:
APPLICANT: Behan, Dominic
APPLICANT: Chalmers, Derick
TITLE OF INVENTION: No. 6107324-Endogenous, Constitutively Activated
TITLE OF INVENTION: No. 6107324-Endogenous, Constitutively Activated
TITLE OF INVENTION: Human Serotonin Receptors and Small Molecule Modulators Therec
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSE: Arena Pharmaceuticals, Inc.
STREET: 6166 Nancy Ridge Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 RDHASLGDSETLSQTELRKKERKKKR------ERKFQANCGIDFIIFWILLF 54
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         29; Indels 18; Gaps
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             14; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNET/AGENT INFORMATION:
NAME: MAIK J. ROSEN
REGISTRATION NUMBER: 39,822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568 3439
INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/29
FILING DATE: April 14, 1999
CLASSIFICATION:
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Chalmers, Derek T
Foster, Richard J
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LENGTH: 458 amino acids
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Matches 23; Conservative
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               23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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US-09-292-071-27
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APPLICANT:
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                    Matches
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; OTHER INFORMATION: Description of Artificial Sequence: No. 6420541el Sequence US-09-767-013-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Behan, Dominic
APPLICANT: Behan, Dominic
APPLICANT: Chalmers, Derick
TITLE OF INVENTION: No. 6420541-Endogenous, Constitutively Activated Human
TITLE OF INVENTION: Serotonin Receptors and Small Molecule Modulators
TITLE OF INVENTION: Thereo
TITLE OF INVENTION: Thereo
TITLE OF INVENTION: Thereo
CURRENT PAPLICATION NUMBER: US/09/767,013
FILE REFERENCE: ARENOS
CURRENT FILING DATE: 2001-01-23
PRIOR FILING DATE: 1999-04-14
NUMBER: OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                    6 RDHASLGDSETLSQTELRKKERKKKR------ERKFQANCGIDFIIFWIFWILLF 54
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                                                                                                                                                                                                                                                                                                                                                                   29; Indels 18; Gaps
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Sequence 33, Application US/09292071
Patent No. 6107324
GENERAL INFORMATION:
APPLICANT: Behan, Dominic
APPLICANT: Chalmers, Derick
TITLE OF INVENTION: No. 6107324-Endogenous, Constitutively Activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18; Gaps
                                                                                                                                                                                                                                                                                                                   12.6%; Score 67; DB 4; Length 458; 27.4%; Pred. No. 7.2; ative 14; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
12.6%; Score 67; DB 4; Length 458;
Best Local Similarity 27.4%; Pred. No. 7.2;
Matches 23; Conservative 14; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         329 ITNIL--SVLC----EKSCNQKL 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 SHHWIQESLLCPPSPKEVTCREML 78
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              REFERENCE/DOCKET NUMBER: 3086-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 431-1703
TELEFAX: (610) 431-4181
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 SHHWIQESLLCPPSPKEVTCREML 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27, Application US/09767013
Patent No. 6420541
GENERAL INFORMATION:
REGISTRATION NUMBER: 27,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                           458 amino acids
                                                                                                                                                                                                                             not relevant
                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-09-032-742-10
                                                                                                                                                                              TYPE: amino acid . STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                             TOPOLOGY:
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LENGTH: 458
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Best Local s
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Human Serotonin Receptors and Small Molecule Modulators I
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TITLE OF INVENTION: No. 6140509-Endogenous, Constitutively Activated Human
TITLE OF INVENTION: Serotonin Receptors And Small Molecule Modulators
TITLE OF INVENTION: Thereof
FILE REFERENCE: AREN0033
CURRENT APPLICATION UNDER: US/09/292,069A
PRIOR APPLICATION NUMBER: 60,090,783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54
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                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/292,071 FILING DATE: April 14, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23; Conservative 16; Mismatches
                                                      ADDRESSEE: Arena Pharmaceuticals, Inc. STREET: 6166 Nancy Ridge Drive CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  349 ITNIM--AVICKES----CNEDVIGALL 370
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                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/112,909
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 60/123,000
PRIOR FILING DATE: 1999-03-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 33, Application US/09292069A Patent No. 6140509
                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: MARK J. ROSEN
REGISTRATION NUMBER: 39,822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 564-5525
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ. ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Behan, Dominic P
Chalmers, Derek T
Foster, Richard J
Glen, Robert C
Lawless, Michael S
Liaw, Chen W
                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Russo, Joseph F
Smith, Julian R
TITLE OF INVENTION: HUNDER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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                                                                                                                                               COUNTRY:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                            STATE:
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Gaps

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Sequence 31, Application US/09292071
Patent No. 6107324
GENERAL INFORMATION:
APPLICANT: Behan, Dominic
APPLICANT: Chalmers, Derick
TITLE OF INVENTION: No. 6107324-Endogenous, Constitutively Activated
TITLE OF INVENTION: Human Serotonin Receptors and Small Molecule Modulators
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 GDSE-----TLSQTELRKKERKKKRERKFQANCGIDFIIFWIFWILLFSHHWIQESLLCP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wisconsin Alumni Research Foundation
APPLICANT: Hitchinson, Charles R.
APPLICANT: Hutchinson, Charles R.
APPLICANT: Kennedy, Jonathan n.m.i
APPLICANT: Kennedy, Jonathan n.m.i
ATILE OF INVENTION: METHOD OF PRODUCING ANTIHYPERCHOLESTEROLEMIC AGENTS
FILE REFERENCE: 960296.95148
CURRENT APPLICATION NUMBER: US/09/215,6948
NUMBER OF SEC ID NOS: 36
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                                                                                                                                                                                                                                                                                                                                                                                                       40 GSDFSTGWIFYIDEEGHHDLVSSVDLPEALSKNHCYYLINGSC--WCVQAY 88
                                                                                                                                                                                                                                                                                                                                                                           40 GIDFIIFWIFWILLFSHHWIQESLLCPPSPKEVTCREMLTGGCLPWATRSH 90
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                                                                                                                                                                                                                                                                         Score 64; DB 4; Length 380;
Pred. No. 13;
9; Mismatches 25; Indels
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PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DAFE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
SEQ ID NOS: 5674
LENGTH: 380
                                                                                                                                                                                                  ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15, Application US/09215694B Patent No. 6391583
                                                                                                                                                                                                                                                                         12.0%;
29.4%;
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patentin Ver. 2.0
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Best Local Similarity 26.68
Matches 17; Conservative
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 29.4;
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92121
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LENGTH: 488
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID ANINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: No. 6420541el Sequence US-09-767-013-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chalmers, Derick
TITLE OF INVENTION: No. 6420541-Endogenous, Constitutively Activated Human
TITLE OF INVENTION: Serotonin Receptors and Small Molecule Modulators
TITLE OF INVENTION: Thereo
FILLE REFERENCE: ARENO35
CURRENT APPLICATION NUMBER: US/09/767,013
PRIOR APPLICATION NUMBER: 09/292,072
PRIOR FILLING DATE: 2001-01-23
PRIOR FILLING DATE: 1999-04-14
SUNMER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: No. 6140509el; OTHER INFORMATION: Sequence
US-09-292-069A-33
                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                  Query Match 12.4%; Score 66; DB 4; Length 478; Best Local Similarity 25.8%; Pred. No. 9.8; Matches 23; Conservative 16; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.4%; Score 66; DB 4; Length 478; 25.8%; Pred. No. 9.8; tive 16; Mismatches 32; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 SHHWIQESLLCPPSPKEVTCREMLTGGCL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 SHHWIQESLLCPPSPKEVTCREMLTGGCL 83
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CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                     6 RDHASLGDSETLSQTELRKKERKKKR--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 33, Application US/09767013; Patent No. 6420541; GENERAL INFORMATION; APPLICANT: Behan, Dominic
                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23; Conservative
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US-09-134-001C-3830
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US-09-767-013-33
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Gaps

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us-09-854-133-586.rai

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FGLEIA NO. 144030

FGREEAL NO. 144030

FARELICANT: Behan, Dominic P

APPLICANT: Chalmers, Derek T

APPLICANT: Chalmers, Derek T

APPLICANT: Law, Chen W

APPLICANT: Law, Chen W

APPLICANT: Liu, Qian

APPLICANT: Russo, Joseph F

APPLICANT: Russo, Joseph F

APPLICANT: Thomsen, William J

TITLE OF INVENTION: Serctonin Receptors And Small Molecule Modulators

TITLE OF INVENTION: Serctonin Receptors And Small Molecule Modulators

TITLE OF INVENTION: Serctonin Receptors And Small Molecule Modulators

TITLE OF INVENTION: Serctonin Receptors And Small Molecule Modulators

TITLE OF INVENTION: Serctonin Receptors And Small Molecule Modulators

TITLE OF INVENTION: Serctonin Receptors And Small Molecule Modulators

TITLE OF INVENTION: NUMBER: 60/090,783

PRIOR FILING DATE: 1999-04-14

PRIOR FILING DATE: 1999-01-18

PRIOR FILING DATE: 1999-03-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 RDHASLGDSETLSQTELRKKERKKKR-------ERKFQANCGIDFIIFWILLF
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11.7%; Score 62; DB 3; Length 478;
Best Local Similarity 24.7%; Pred. No. 29;
Matches 22; Conservative 16; Mismatches 33; Indels 18; Gaps
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FPLICATION NUMBER: US/09/292,071
FILING DATE: April 14, 1999
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   349 ITNIM--AVICKES----CNEDVIGALL 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 31, Application US/09292069A Patent No. 6140509
                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: MARK J. ROSEN
REGISTRATION NUMBER: 39,822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 564-6525
TELERAX: (215) 568-3439
INPORMATION FOR SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           not relevant
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; MOLECULE TYPE: protein
US-09-292-071-31
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US-09-292-069A-31
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6 RDHASLGDSETLSQTELRKKERKKKR------ERKFQANCGIDFIIFWIFWILLF 54
                                         18;
11.7%; Score 62; DB 4; Length 478; ilarity 24.7%; Pred. No. 29; Conservative 16; Mismatches 33; Indels
                                                                                                                                                                                 349 ITNIM--AVICKES----CNEDVIGALL 370
                                                                                                                                                             55 SHHWIQESLLCPPSPKEVTCREMLTGGCL 83
                                                                                                                                                                                                                                                            Search completed: July 9, 2003, 15:08:26 Job time: 35.0443 secs
  Query Match
Best Local Similarity
Matches 22; Conserv
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July 9, 2003, 15:06:38; Search time 32.6195 Seconds (without alignments) 346.196 Million cell updates/sec
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GenCore version 5.1.6 copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                445758 seqs, 116419773 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published_Applications_AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                        OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                   Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
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pred. No. is the number of results predicted by chance to have a	score greater than or equal to the score of the result being princed,	and is derived by analysis of the total score distribution.	
Pred. N	Score d	מי ליים	210

	Description		Seguence 586, App		•			Sequence 587, App		Sequence 400, App		Adv 100+ anhas	Sednence 0730, Ap	Sequence 1089, Ap	compande 2. Appli	tradition of the same	Sednence 730, App	Sequence 126, App	Sequence 16, Appl	Segmence 40. Appl	•	Sednence 4730, Ap	~	Segmence 291, App	
	ID	ns-09-854-133-586	TTC-10-144-6492-586	000 WCBO ##T-OT-CO	08-5/6-86/-60-SD	US-10-144-649A-742	US-09-854-133-587	US-10-144-649A-587	US-09-738-973-587	007-22-00-80-51	001 001 010 60 60	US-09-948-783-400	US-10-106-698-6236	118-09-764-877-1089		US-09-903-396A-2	US-10-251-385-230	US-10-251-385-126	TTG-10-225-567A-16		08-170-298-60-SD (US-09-764-891-4290	118-09-838-955-3	107-107-001	T67-T60-76T-0T-S0
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US-09-866-050A-673 US-09-801-368-24	US-10-001-83/-133 US-09-864-761-38925	US-09-864-7					US-09-877-843-40	US-09-883-343A-71	TIC-10-242-943-4	TS-10-060-795B-3	US 10 000 7,55 5		US-U9-/04-004-1	US-10-280-858-1			US-10-280-858-7		-	rrc-10-280-858-13	TO 10 10 10 10 10 10 10 10 10 10 10 10 10	US-IU-200 030 IV	258-087-07	US-10-280-858-21	US-10-280-858-23	
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ALIGNMENTS

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                                                                         APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Dirin R.
APPLICANT: Henderson, Darin R.
APPLICANT: Benson, Darin R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CURRENT PLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2101-10-11
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 100.0%; Score 532; DB 9; Length 97;
Best Local Similarity 100.0%; Pred. No. 1e-48;
Matches 97; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 586, Application US/10144649A publication No. US20030118599A1 GENERAL INFORMATION: APPLICANT: Lodes, Michael J.
US-09-854-133-586
VS-09-854-133-586
Sequence 586, Application US/09854133
Publication No. US20020183499A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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US-10-144-649A-586
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US-09-854-133-586
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LENGTH: 97
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0
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.476C11
CURRENT APPLICATION NUMBER: US/10/144,649A
NUMBER OF SEQ ID NOS: 749
SOUTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                             100.0%; Score 532; DB 9; Length 97; 100.0%; Pred. No. 1e-48; tive 0; Mismatches 0; Indels
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APPLICANT: Mannion, Jane
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475c9
CURRENT APPLICATION NUMBER: US/09/738,973
CURRENT FILIG DAFE: 2000-12-14
NUMBER OF SEQ ID NOS: 587
SOFTWARE: FASTSEQ FOR Windows Version 3.0
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Secrist, Heather
Indirias, Carol Yoseph
Benson, Darin R.
Elliot, Mark
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Henderson, Robert A.
Lodes, Michael J.
Fling, Steven P.
Mohamath, Raodoh
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US-10-144-649A-586
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ORGANISM: Homo sapiens
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APPLICANT: Reed S
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US-09-738-973-586
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SEQ ID NO 586
LENGTH: 97
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LENGTH: 97
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APPLICANT:
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APPLICANT:
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                                                                              APPLICANT: Lodes, Michael J.
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475c11
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 749
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lodes, Michael J.
APPLICANT: Modamath, Raodoh
APPLICANT: Modamath, Raodoh
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Darin R.
APPLICANT: Benson, Darin R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
SOFTWARE FEING DATE: 2001-05-11
SOFTWARE: FastSEQ for Windows Version 3.0
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1 Similarity 100.0%; Pred. No. 1.2e-48;
97; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.00064;
tive 0; Mismatches 0;
                    ; Sequence 742, Application US/10144649A; Publication No. US20030118599A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 587, Application US/09854133
; Publication No. US20020183499A1
; GENERAL INFORMATION:
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Best Local Similarity 100.C
Matches 16; Conservative
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US-09-854-133-587
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Best Local Similarity
Matches 97; Conserve
US-10-144-649A-742
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US-10-144-649A-587
                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 742
                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 114
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APPLICANT: Lodes, Michael J.
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Momell, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER
CURRENT APPLICATION UNMBER: US/10/144,649A
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 749
SOFTWARE: FastEQ for Windows Version 3.0
SEQ ID NOS: 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mannion, Jane
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.4%; Score 98; DB 10; Length 16; 100.0%; Pred. No. 0.00064; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                    Score 98; DB 9; Length 16; Pred. No. 0.00064;
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Publication No. US2003007780941
GENERAL INFORMATION:
TITLE OF INVENTION: 97 Human secreted proteins
                                                                                                                                                                                                                                                                                              18.4%; Scor.
100.0%; Pred. No. v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Algate, Paul A.
Secrist, Heather
Indirias, Carol Yoseph
Benson, Darin R.
Elliot, Mark
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Lodes, Michael J.
Fling, Steven P.
Mohamath, Raodoh
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Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.0
Matches 16; Conservative
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NUMBER OF SEQ ID NOS: 587
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; ORGANISM: Homo sapiens
US-09-738-973-587
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APPLICANT:
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LOCATION: (110) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Where Introduction: Xaa equals any of the naturally occurring L-amino acids NAME/REY: SITE
LOCATION: (52)
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CURRENT APPLICATION NUMBER: US/09/892,877
CURRENT APPLICATION NUMBER: US/09/437,658
CURRENT FILING DATE: BARLIER APPLICATION NUMBER: US/09/437,658
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-11-10
PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 400
LENGTH: 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ruben et. al. TITLE OF INVENTION: 97 Human secreted proteins FILE REFERENCE: PZ028P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/948,783
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/231,846
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PRIOR FILING DATE: 2001-09-18
PRIOR FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: 09/437,658
PRIOR FILING DATE: 1999-11-10
PRIOR PELICATION NUMBER: PCT/US99/09847
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PRIOR PELLING DATE: 1998-05-12
PRIOR PELLING DATE: 1998-05-12
PRIOR PELLING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/085,927
PRIOR APPLICATION NUMBER: 60/085,906
PRIOR FILING DATE: 1998-05-18
PRIOR FILING DATE: 1998-05-18
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DR APPLICATION NUMBER: 60/085,093
DR FILING DATE: 1998-05-12
DR APPLICATION NUMBER: 60/085,094
DR FILING DATE: 1998-05-12
DR APPLICATION NUMBER: 60/085,105
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PRIOR APPLICATION NUMBER: 60/085,921
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,923
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APPLICATION NUMBER: 60/085,924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 400, Application US/09948783 publication No. US20030100051A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-948-783-400
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271 TIGDVTTEQYLALR---RKKKTTVKMLVLVVVLEALCWFPLNCYVLLLSSKAIHTNNALY 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Allen, Keith D. TITLE OF INVENTION: TRANSGENIC MICE CONTAINING TITLE OF INVENTION: GLUCOCORTICOID-INDUCED RECEPTOR GENE DISRUPTIONS FILE REFERENCE: R-359
                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
SOFTWARE PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 50.0%; Pred. No. 2.8;
Matches 19; Conservative 5; Mismatches 7; Indels
                                        Sequence 1089, Application US/09764877
Patent No. US20020147140A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE. REFERENCE: PC005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match. 12.8%; Score 68; DB 9; Length 423; Best Local Similarity 22.8%; Pred. No. 29; Matches 29; Conservative 11; Mismatches 41; Indels
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CURRENT FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/217,179
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2010-11-6
PRIOR FILING DATE: 2010-11-6
PRIOR FILING DATE: 2010-11-6
SPRIOR FILING DATE: 2001-11-6
SOFTWARE: FRSELEQ for Windows Version 4.0
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; Publication No. US20030105292A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo saplens
US-09-764-877-1089
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                                                                                                                                                                                                                                                                 SEQ ID NO 1089
LENGTH: 66
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US-09-903-396A-2
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LENGTH: 423
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TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REPERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
PRIOR APPLICATION NUMBER: US/27
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-11-03
PRIOR FILING DATE: 1999-11-03
                                                                                                                                                                                                                                                                                                       LOCATION: (46)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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LOCATION: (52)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Best Local Similarity 27.4%; Pred. No. 0.37;
Matches 29; Conservative 9; Mismatches 21; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 13.4%; Score 71.5; DB 9; Length 163; 22; Conservative 5; Mismatches 9; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 HWIQESLLCPPSPKEVTCREML/GGCLPWA-----TRSHLGRRKC 96
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,925
PRIOR FILING DATE: 1998-05-18
PRIOR PLING DATE: 1998-05-18
PRIOR PLING DATE: 1998-05-18
PRIOR FILING DATE: 1998-05-18
PRIOR FILING DATE: 1998-05-18
PRIOR FILING DATE: 1998-05-18
SOFTWARE: PAGO ID NOS: 465
SOFTWARE: PAGENTIN Ver. 2.0
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Publication No. US20030109690A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEO ID NOS: 8564
SOFTWARE: PatentIn Ver. 3.0
                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens US-10-106-698-6236
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Matches 22; Conserva
                                                                                                                                                                                                                                                                                    NAME/KEY: SITE
LOCATION: (46)
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US-09-764-877-1089
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LENGTH: 163
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sequence 126, Application US/10251385

publication No. US20030105292A1

general involvantion No. US20030105292A1

APPLICANT: Behan, Dominic P.

APPLICANT: Chalmers, Derek T.

APPLICANT: Chalmers, Derek T.

TITLE OF INVENTION: Protein-Coupled

TITLE OF INVENTION: Receptors

FILE REFERRNCE: AREN 0040

CURRENT FILING DATE: 2002-09-20

PRIOR APPLICATION NUMBER: US/10/251,385

CURRENT FILING DATE: 1998-10-13

NUMBER OF SEQ ID NOS: 294

SOFTWARE PATELLY OF NOS: 294

SOFTWARE PATELLY OF NOS: 294

SOFTWARE PATELLY OF NOS: 294
APPLICANT: Behan, Dominic P.

APPLICANT: Chalmers, Derek T.

APPLICANT: Chalmers, Derek T.

APPLICANT: Liaw, Chen W.

TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

TITLE REFERENCE: AREN-0040

CURRENT APPLICATION NUMBER: US/10/251,385

CHRENT APPLICATION NUMBER: US/09/170,496

PRIOR FILING DATE: US/09/170,496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 RDHASLGDSETLSQTELRKKERKKKR------ERKFQANCGIDFIIFWILLF 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 12.8%; Score 68; DB 9; Length 458; Best Local Similarity 27.4%; Pred. No. 31; Matches 23; Conservative 15; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            329 ITNIL--SVLC----EKSCNOKL 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 SHHWIQESLLCPPSPKEVTCREML 78
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                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-10-251-385-126
                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-225-567A-16
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US-10-251-385-126
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LENGTH: 458
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APPLICANT: LIFESPANTION:
APPLICANT: Burmer, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Burmer, Clenna C.
APPLICANT: Burmer, Clenna C.
APPLICANT: Burmer, Clenna C.
APPLICANT: Burmer, Clenna C.
APPLICANT: Roush, Christine L.
APPLICANTON NUMBER: US/10/225,567A
CURRENT FILING DATE: 2000-12-19
CURRENT FILING DATE: 2000-12-19
RIOR PRICH FLING DATE: 2000-12-19
CURRENT FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
CURRENT FILING DATE: 2000-12-19
SOCTWARE: PAT
AVERE: PAT
AVE: PAT
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 9, 2003, 15:05:28 ; Search time 43.7788 Seconds Run on:

(without alignments)
213.004 Million cell updates/sec

US-09-854-133-586 Perfect score:

1 EVEVSRDHASLGDSETLSQT.....LTGGCLPWATRSHLGRRKCS 97 Sednence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

283224 Total number of hits satisfying chosen parameters:

283224 segs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		hypothetical prote	glucocorticoid-ind	glucocortico1d-ind	glucocorticoid-ind	glucocorticoid-ind	erotonin receptor	hypothetical prote	variant-specific s	hypothetical prote	artifact-warning s	ycdy protein homol	probable oxidoredu	probable oxidoredu	cytochrome P450 CY	Ca2+-transporting	rotein H28G03.3 [H+-transporting tw		30S ribosomal prot	probable bacteriop	-	hypothetical prote	_		ist	trichohyalin - she	hypothetical prote	protein B0272.5 [i
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	a	A82037	T32024	A40470	B40470	D40470	C40470	JS0616	T19964	B71600	T49635	F40201	A64915	A90916	F85764	T08014	A48770	G89530	806079	AB3061	E98225	B83131	T14029	T27655	T25366	T19520	T49196	0	T18688	689608
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	Query Match Length	177	684	381	423	443	491	458	1851	2197	132	673	207	207	207	514	163	199	177	266	572	728	2228	326	350	356	428	1549	1555	1973
æ	Query	13.6	13.2	12.8	ď	12.8	12.8	12.6	12.6	ς.	12.4	12.4	12,3	12.3	12.3	12.2	12.1	12.0	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	ij.	11.7	11.7	11.7
	Score	72.5		69	89	89	69	67	67	66.5	99	99	65.5	65.5	65.5	65	64.5	64	62.5	62.5	62.5	62.5	62.5	62	62	62	62	62	62	62
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118686 115571 189608 1423329 1423329 1423329 142881 16014 17281 1751275 175127
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### ALIGNMENTS

	Imported
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	subunit
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_	thase

RESULT A82037

1] - Vibrio cholerae (strain N16961 se our species: Vibrio cholerae C.Species: Vibrio cholerae C.Species: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 ATP syn

C; Accession: A82037

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, I chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Selles I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Fitle: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Fitle: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A; Accession: A82037

A;Status: preliminary A;Molecule type: DNA A;Rossidues: 1-177 <HEI>> A;Cross-references: GB:AE004342; GB:AE003852; NID:g9657358; PIDN:AAF95906.1; GSPDB: A;Experimental source: serogroup 01; strain N16961; biotype El Tor

C;Genetics: A;Gene: VC2767

A;Map position: 1 C;Superfamily: H+-transporting ATP synthase delta chain

Gaps 7; Query Match
13.6%; Score 72.5; DB 2; Length 177;
Best Local Similarity 32.6%; Pred. No. 0.79;
Matches 15; Conservative 11; Mismatches 13; Indels 7

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4 VSRDHASLGDSETLSQTELRKKER-----KKKRERKFQANCGID 42 ŏ

Dp

RESULT 2

hyporhetical protein T06D4.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Accession: T32024

Rile, T.T.; Goela, D. submitted to the EMBL Data Library, July 1997 submitted to the EMBL Data Library, July 1997 A;Description: The sequence of C. elegans cosmid T06D4. A;Reference number: Z21113 A;Reference number: Z21113

A Molecule type: DNA A; Residues: 1-684 <LET> A; Cross-references: EMBL: AF016673; PIDN: AAB66123.1; GSPDB:GN00020; CESP: T06D4.4 A; Experimental source: strain Bristol N2; clone T06D4

A; Gene: CESP:T06D4.4

A;Map position: 2 A;Introns: 75/3; 121/1; 150/3; 183/1; 227/3; 319/3; 357/3; 408/1; 444/3; 497/1; 62

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C; Species: Mus musculus (house mouse)
C; Dete: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 20-Apr-2000
C; Dete: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 20-Apr-2000
C; Accession: D40470
R; Harrigan, M.T.; Campbell, N.F.; Bourgeois, S.
Mol. Endocrinol. 5, 1331-1338, 1991
A; Title: Identification of a gene induced by glucocorticoids in murine T-cells: a p. A; Reference number: A40470; MUID: 92123228; PMID:1663214
A; Accession: D40470
A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-443 < CHAR>
A; Cross-references: GB: M80160
C; Superfamily: neurokinin 1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glucocorticoid-induced receptor, long form RP82 - mouse C.Species: Mus musculus (house mouse) C.Species: Mus musculus (house mouse) C.Date: 14-Feb-1992 #text_change 20-Apr-2000 C.Accession: C40470 R.Harrigan, M.T.; Campbell, N.F.; Bourgeois, S. Mol. Endocrinol. 5, 1331-1338, 1991 A.Title: Identification of a gene induced by glucocorticoids in murine T-cells: a pc A.Reference number: A40470; MUID:92123228; PMID:1663214 A.Stellininary
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348 FAFHWFAMSSTCYNPFIYCWLNENFRVELKALLSMCQRPPKPQEDRLPSPVPSFRVAWTE 407
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                                                                                                                                                         glucocorticoid-induced receptor, long form RP105 - mouse
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Local Similarity 22.8%; Pred. No. 6.4;
hes 29; Conservative 11; Mismatches
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C;Superfamily: neurokinin 1 receptor
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                                        388 KSH-GRR 393
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RSHLGRR 94
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456 KSH-GRR 461
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Best Local Similarity
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A; Residues: 1-491 <HAR>
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R;Harrigan, M.T.; Campbell, N.F.; Bourgeois, S.
Mol. Endocrinol. 5, 1331-1338, 1991
A;Title: Identification of a gene induced by glucocorticoids in murine T-cells: a potent A;Reference number: A40470; MUID:9212328; PMID:1663214
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-381 <ARS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glucocorticoid-induced receptor precursor, short form RP23 - mouse C.Species: Mus musculus (house mouse) C.Species: Mus musculus (house mouse) C.Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 20-Apr-2000 C.Accession: B40470 R.Harrigan, M.T.; Campbell, N.F.; Bourgeois, S. A. Harrigan, M.T.; Campbell, N.F.; Bourgeois, S. A. Filte: Identification of a gene induced by glucocorticoids in murine T-cells: a potent A.Reference number: A40470; MUID:92123228; PMID:1663214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-423 <HAR>
A;Cross-references: GB:M80481; GB:M80610; NID:g193516; PIDN:AAA17882.1; PID:g460318
C;Superfamily: neurokinin 1 receptor
                                                              1;
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C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 SLGDSETLSQTELRKKERKKKRERKFQANCGIDFIIFWI---FWILL-------
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              Length 684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.8%; Score 68; DB 2; Length 381; 22.8%; Pred. No. 5.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 12.8%; Score b8; DB 2; Denyth 22.8%; Pred. No. 5.6;
Matches 29; Conservative 11; Mismatches 41; Indels
                                                         9; Indels
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                                                                                           23 RKKERKKKRERKFQA-----NCGIDFIIFWIFWILLF 54
                                                                                                                          DB 2;
       Score 70; DB 2
Pred. No. 5.8;
9; Mismatches
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C;Superfamily: neurokinin 1 receptor
       13.2%;
31.8%;
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Best Local Similarity 22.8%;
Query Match 13.2
Best Local Similarity 31.8
Matches 14; Conservative
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A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Accession: B71600
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A;Experimental source: clone 3D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Species: Neurospora crassa
C.Jaceste: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
C.Jacession: T44635
R.Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyaka
submitted to the Protein Sequence Database, May 2000
A;Reference number: 225022
A;Accession: T49635
A;Status: preliminary
                                                                                                                                                            Cjaccession: B71600
R;Gardner, M.J; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, R; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, Science 282, 1126-1132, 1998
variant-specific surface protein 1 homolog PFB1055c - malaria parasite (Plasmodium N;Alternate names: erythrocyte membrane binding protein 1 (EMP1) C;Species: Plasmodium falciparum C;Species: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                602 EVQKVKDDKN-GEEEDEDEEDVDKVKKAGGLCILENKKHESRNNSSNEPEQFQKTFHDFF 660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37 SSVTTTRIWGRKEKKKKKKRRKKRTEQGNAKDGDTTVNADGQRSVVGWLVGFWPSLHHHAA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVEVSRDHASLGDSETLSQTELRK------KERKKKRERKFQAN-----CGIDFI 44
                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   artifact-warning sequence (translated ALU class F) - human
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
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A;Residues: 1-132 <SCH>
A;Cross-references: EMBL:AL355932; GSPDB:CN00116; NCSP:B5022.170
A;Experimental source: BAC clone B5022; strain OR74A
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 6
C;Superfamily: Neurospora crassa hypothetical protein B5022.170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15; Mismatches
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A; Residues: 1-2197 <GAR>
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Best Local Similarity
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A; Map position: Xq24-Xq24
C; Superfamily: vertebrate rhodopsis : Though of receptor; glycoprotein; neurotransmitter receptor; transmed : Seyberfamily: vertebrate receptor; glycoprotein; neurotransmitter receptor; transmembrane #status predicted <TM1>
F; 52-78/Domain: transmembrane #status predicted <TM2>
F; 128-149/Domain: transmembrane #status predicted <TM3>
F; 121-194/Domain: transmembrane #status predicted <TM4>
F; 121-334/Domain: transmembrane #status predicted <TM4>
F; 121-333/Domain: transmembrane #status predicted <TM6>
F; 349-370/Domain: transmembrane #status predicted <TM6>
F; 340-370/Domain: tran
                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Mesidues: 1-458 cSAL.>
A; Cross-references: GB:M81778; NID:g338027; PIDN:AAA60317.1; PID:g338028
C; Comment: This receptor protein is membrane-bound and couple to G-proteins, which activ
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A;Map position: 4
A;Introns: 15/3; 42/1; 65/2; 93/3; 239/2; 340/1; 448/3; 863/3; 1096/3; 1351/3; 1495/3;
        Serotonin receptor 1C - human

N;Alternate names: 5-hydroxytryptamine receptor 1C (5-HTR1C)

C;Species: Homo sapiens (man)

C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 13-Aug-1999

C;Accession: JS0616

R;Saltzman, A.G.; Morse, B.; Whitman, M.M.; Ivanshchenko, Y.; Jaye, M.; Felder, S. Biochem: Biophys. Res. Commun. 181, 1469-1478, 1991

A;Fitle: Cloning of the human serotonin 5-HTZ and 5-HTIC receptor subtypes.

A;Reference number: JS0615; MUID: 92109767; PMID: 1722404
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A; Cross-references: EMBL:Z68296; PIDN:CAA92591.1; GSPDB:GN00022; CESP:C46C2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 RDHASLGDSETLSQTELRKKERKKRR------ERKFQANCGIDFIIFWIEWILLF 54
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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Matches 23; Conservative 14; Mismatches
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C:Species: Escherichia coll
Especies: A.Rej Species: A
                                                                                                                                                   A Molecule type: DNA
A Residues: 1-673 <CLA>
R:Claverie, J.M.
Genomics 12, 838-841, 1992
A:Title: Identifying coding exons by similarity search: Alu-derived and other potentiall
A:Reference number: A40200; MUID:92241891; PMID:1572661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C'Accession: A90916
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasumaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genchine number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                   A:Contents: annotation C:Comment: This "warning" entry is a conceptual translation in all 6 reading frames of in-frame stop codons are shown as 'X'.
C:Comment: Any significant similarity of a predicted protein sequence to a portion of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable oxidoreductase component ECs2297 [imported] - Escherichia coli (strain 0157:H7)
C.Species: Escherichia coli
C.bate: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ñ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 ASLGDSETLSQTELRKKERKKKRERKFQANCGIDFIIFWIFWILLFSHHWIQESLLCPPS 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VEVSRDHASLGDSETLSQTELRKKERKKKRERKFQANCGIDFIIFWIFWILLFSHHWIQE 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
12.4%; Score 66; DB 4; Length 673;
Best Local Similarity 21.3%; Pred. No. 17;
Matches 19; Conservative 17; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33; Indels
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28.7%; Pred. No. 5.9;
ive 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364 PAGV-----CS 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 PKEVICREMLIGGCLPWATRSHLGRRKCS 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 ----NGROTECEELLAWHLFPWSTR 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 SLLCPPSPKEVTCREMLTGGCLPWATR 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 28.78
Matches 25; Conservative
                                          personal communication, 1992
                                                                               A; Reference number: A40201
A; Accession: F40201
R;Claverie, J.M.
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probable oxidoreductase component 22581 [imported] - Escherichia coli (strain 0157: C.Species: Escherichia coli (c.Species: E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apo Nature 409, 529-533, 2001
A.Filler: Genome sequence of enterohemorrhagic Escherichia coli (o157:H7. A. A. Reference number: A85480; MUID:21074935; PMID:11206551
A. Reference number: A85480; MUID:21074935; PMID:11206551
A. Residues: 1-207 <sro>
A. Residues: 1-207 <sro>
A. Residues: 1-207 <sro>
A. Experimental source: strain (o157:H7, substrain EDL933)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytochrome P450 CYP94A1 - spring vetch
Cytochrome P450 CYP94A1 - spring vetch
Cyspecies: Vicia sativa (spring vetch, tare)
Cyspecies: 21-May-1999 #sequence_revision 21-May-1999 #text_change 16-Feb-2001
Cytocession: T08014
RyTijet, N.; Helvig, C.; Pinot, F.; le Bouquin, R.; Lesot, A.; Durst, F.; Salaun, J.
Biochem J. 332, 583-589, 1998
AyTitle: Functional expression in yeast and characterization of a clofibrate-inducib
AyReference number: Z16287; MUID:98264856; PMID:9601090
AyAccession: T08014
AyStaus: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4,
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-207 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB35720.1; PID:g13361763; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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                                                                                                                                                                                                                                                                                                  DB 2; Length 207;
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                                                                                                                                                                                                                                                                                           12.3%; Score 65.5; Di 28.7%; Pred. No. 5.9;
                                                                                                                                                                                                                                                                                                                                                          14; Mismatches
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28.7%; Pred. No. 5.9;
tive 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 -----NGROTECEELLAWHLFPWSTR 164
                                                                                                                                                                                                                      C; Superfamily: Escherichia coli ycdy protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 SLLCPPSPKEVTCREMLTGGCLPWATR 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Superfamily: Escherichia coli ycdy protein
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                                                                                                                                                                                                                                                                                                                      Best Local Similarity 28.78
Matches 25; Conservative
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Best Local Similarity
Matches 25; Conserva
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                                                                                                                                                                                               A; Gene: ECs2297
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                                                                                                                                                                                                                                                                                           Query Match
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F85764
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Search completed: July 9, 2003, 15:09:44 Job time: 46.7788 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 9, 2003, 15:05:28; Search time 12.0177 Seconds (without alignments) 334.773 Million cell updates/sec Run on:

US-09-854-133-586 532 1 EVEVSRDHASLGDSETLSQT.....LTGGCLPWATRSHLGRRKCS 97 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	31 mus mus		_	081117 vicia sativ		P12987 vibrio algi	Q9hwr3 pseudomonas						P29430 pediococcus	mus mu	human		mus mu				P50407 cavia porce		P32305 rattus norv			-	Q92793 homo sapien	P47148 saccharomyc	606	057457 brachydanio	7	665 drosc	P02787 homo sapien
SUMMARIES	ID	GP72_MOUSE	5H2C_HUMAN	YNFI_ECOLI	C941_VICSA	APJ_XENLA	ATPD_VIBAL	BPHY_PSEAE	TRHY_SHEEP	ACD1_CLOPE	5H7_HUMAN	RS1_RHIME	POLG_HRV89	PPA1_PEDAC	ETS2_MOUSE	VE4_HPV11	VE4_HPV6C	5H2C_MOUSE	CBF5_YEAST	MYOG_CHICK	ANR2_HUMAN	5H7_CAVPO	5H7_MOUSE	5H7_RAT	HH1R_HUMAN	ACM3_CHICK	CBP_MOUSE	CBP_HUMAN	YJ81_YEAST	5H2C_RAT	NBL4_BRARE	ICAL_RAT	SRYB_DROME	TRFE_HUMAN
	Length DB	423						728 1							89	80	80	59	83	27	33	446 1	48									_		698 1
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P56566 mus musculu	P53724 saccharomyc	O14966 homo sapien	Q28509 macaca mula	P40986 saccharomyc	P11267 simian immu	P91620 drosophila	P91621 drosophila	Q9wv06 mus musculu	P38487 bacillus sp	Q8vc56 mus musculu	P38361 saccharomyc
S103_MOUSE	YN8C_YEAST	RB7L_HUMAN	B2AR_MACMU	CC1_YEAST	ENV_SIVML	SIF2_DROME	SIF1_DROME	ANR2_MOUSE	CREA_BACSP	RNF8_MOUSE	YB8I_YEAST
1	-	7	Н	Н	Н	Н	٦	-	Н	Н	П
101	139	203	415	491	880	2044	2064	328	410	488	574
10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.8	10.8	10.8	10.8
58	28	28	28	28	28	28	28	57.5	57.5	57.5	57.5
			_	m	39	0	11	~1	<u></u>	-*	10

# ALIGNMENTS

423 AA.	sequence update)	or GFK/Z precursor (Glucocorticola-	ists. Wortobrats. Ditolonatomi.	Craniata; Vertebrata; Euteleoscomi; Sciurognathi; Muridae; Murinae; Mus.			geois S.;	"Identification of a gene induced by glucocorticoids in murine	:	ORPHAN RECEPTOR, COULD BE A NEUROPEPTIDE Y RECEPTOR. AR LOCATION: Integral membrane protein.		MUS AND SPLEEN.	INDUCTION: BY GLUCOCORTICOIDS AND CAMP; IN T-CELLS.	SIMILARITY: BELONGS TO FAMILY I OF G-PROTEIN COUPLED RECEPTORS.	This SWISS-PROT entry is copyright. It is produced through a collaboration	between the Swiss Institute of Bioinformatics and the EMBL outstation -		ed. Usage by and for commerc	agreement (See http://www.isb-sib.ch/announce/ ish-sib_ch)						.kECEP_rl_z; 1. Transmembrane: Glycoprotein: Signal;		POTENTIAL.	9	TYTRACELLULAR (POTENTIAL).	CYTOPLASMIC (POTENTIAL).	2 (POTENTIAL). EXTRACELLULAR (POTENTIAL).	3 (POTENTIAL).
.RD; PRT;				Chordata; Cran Rodentia; Sciu		. N. CC 2214	MEDLINE=92123228; PubMed=1663214; Harrigan M.T., Campbell N.F., Bourgeois S.;	gene induced	Mol. Endocrinol. 5:1331-1338(1991).	FUNCTION: ORPHAN RECEPTOR, COULD BE A NE SUBCELLULAR LOCATION: Integral membrane	CTS: MULTIPLE	ING. Y: BRAIN, THY	COCORTICOIDS	SIMILARITY: BELONGS TO FAMILY	is copyright	stitute of Bi	institutions as long	statement is not	requires a license agreement (So		2.1;	InterPro, IPR000276; GPCR_Rhodpsn.	I.	G_PROTEIN_RECEP_F1_1;	G_PROTEIN_RECEP_ receptor: Transm		~	•				
STANDARD;	3 (Rel. 25, 5 (Rel. 32, 1 (Rel. 40,	G protein-coupled eceptor). Grb			=10090;	ROM N.A.	.I., Campbe	ation of a	rinol. 5:13	ON: ORPHAN LULAR LOCAT	ATIVE PRODU	ATIVE SPLICING. SPECIFICITY: B	ION: BY GLU	KITY: BELON	-PROT entry	he Swiss Ir	an Bioinio on-profit	,,,	equires a ]		M80481; AAA17882.1;	IPR000276;	001; /tm_1; 00237: GDCE	S00237; G_F		s splicing.	11,		18 71	93 10		146 167
RESULT 1 GP72_MOUSE ID GP72_MOUSE AC P30731;	01-APR-1993 01-APR-1993 01-NOV-1995 16-OCT-2001	Probable G procein induced receptor). GDB72 OP GIP	Mus musculus	Eukaryota; Metazoa; Mammalia; Eutheria;	NCBI_TaxID=10090; [1]	SEQUENCE FROM N.A.	MEDLINE=9212322 Harrigan M.T.,	"Identific	Mol. Endoci	-!- FUNCTION: -!- SUBCELLULA		ALTERNATIVE -!- TISSUE SPECI	,	-i- SIMILA	This SWISS	between the	use by non-profit	modified an	entities requires	; ;	EMBL; M80481; AAA1781 MGD: MGT:95712: Gir	InterPro;	Pram; Pruo( Delwrs: De(	PROSITE; PS00237; G_PROTEIN_RE	PROSITE; PS50262; G-protein coupled	Alternative splicing	SIGNAL	CHAIN	DOMAIN	DOMAIN	TRANSMEM	TRANSMEM
RESULT GP72_M ID G	01 01	E E	SSS	388	R OX	RP	R'A	RT	R.	ខ្លួ	ខ	88	8	3 5	38	ខ្លួ	ខ្លួ	ຍ	္ပင္	ខ	DR PR	D. S.	y c	DR.	K DK	KW	FT	F	• E- E	FF	F	FT

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5;
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7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

BY SIMILARITY.

MISSING (IN ISOFORM RP39).

Q -> QGLTAIAVDRHQGLELQKMVRPRGDGGELRSPSVTF
                                                                                                                                                                                                                                                                                                                                                    327
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                                                                                                                                                                                                                                                                                                                                                                            271 TIGDVTTEQYLALR --- RKKKTTVKMLVLVVVLFALCWFPLNCYVLLLSSKAIHTNNALY
                                                                                                                                                                                                                                                                                                                      10 SLGDSETLSQTELRKKERKKKRERKFQANCGIDFIIFWI---FWILL-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning of the human serotonin 5-HT2 and 5-HT1C receptor subtypes."; Biochem. Biophys. Res. Commun. 181:1469-1478(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stam N.J., Vanderheyden P., Van Alebeek C., Klomp J., De Boer T., Van Delft A.M.L., Olijve W.; "Genomic organisation and functional expression of the gene encoding the human serotonin 5-H12C receptor."; Paramacol. 269:339-348(1994).
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                 Q -> QRPWDFQESQSLHDTLFPPLE (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryora, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saltzman A.G., Morse B., Whitman M.M., Ivanshchenko Y., Jaye M., Felder S.;
                                                                                                                                                                                                                                                                                                 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | SH2C_HUMAN | STANDARD; | PRT; | 458 AA. |
PP28335; | Q9MP28; |
O1-DEC-1992 (Rel. 24, Last sequence update) |
O1-DEC-1992 (Rel. 24, Last sequence update) |
I5-UNN-2002 (Rel. 41, Last annotation update) |
5-hydroxytryptamine 2C receptor (5-HT-2C) (Serotonin receptor) (5HT-1C).
                                                                                                                                                                                                                                                                 'Match 12.8%; Score 68; DB 1; Length 423; Local Similarity 22.8%; Pred. No. 3.8; les 29; Conservative 11; Mismatches 41; Indels
               EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                         3ACE43452BF15391 CRC64;
                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E., Zhao L., Levine A.J., Shenk T., Chang L.-S.;
                           5 (POTENTIAL).
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                                                      6 (POTENTIAL)
                                                                                                                                                                                                                              RP105)
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MEDLINE=95203331; PubMed=7895773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97001158; PubMed-8812491;
                                                                                                                                                                                                                                           48136 MW;
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2388
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KSH-GRR 393
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                                                                                                                                                                                                                                        423 AA;
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                                        DOMAIN
TRANSMEM
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TRANSMEM
                                                                 DOMAIN
            DOMAIN
                                                                                           DOMAIN
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A VICKAUDE JOYATES, FARMENTS, FARMENTS, CARDENS, CARDINA, CARDINA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODDPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism; Multigene family; RNA editing.
                                                                                                                                                                                              RNA editing events within the
'The human serotonin 5-HT2C receptor: complete cDNA, genomic
                                                                                                                                                                                                                                                                                                                 Kalicki J., Mead K.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                           structure, and alternatively spliced variant.";
                                                                                                                                                                       R.B.;
                                                                                                                                                                     Niswender C.M., Sanders-Bush E., Emeson "Identification and characterization of
                                                                                                                                                                                                                    5-HT2C receptor.";
Ann. N.Y. Acad. Sci. 861:38-48(1998).
                                                                                                 SEQUENCE FROM N.A., AND RNA EDITING
                                                                                                                          TISSUE=Brain;
MEDLINE=99127198; PubMed=9928237;
                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96044432; PubMed=7557992;
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                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-116 FROM N.A.
                                               Genomics 35:551-561(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; JS0616; JS0616.
Genew; HGNC:5295; HTR2C.
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DOMAIN
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269 RNTAEEENSANPNODONARRKKKERRPRGTMOAINNERKASKVLGIVFFVFLIMWCPFF 328
                                                                                                                                                                                                                                                                                                             6 RDHASLGDSETLSQTELRKKERKKKR------ERKFQANCGIDFIIFWIFWILLF 54
                                                                                                                                                                                                                                                                                  18; Gaps
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MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alton N. C. Sabar T., Fujita K., Hayashi K., Inada T., Isono K., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Alba H., Baba T., Fujita K., Hayashi K., Isasai H., Kasai H., Kashi H., Kashi M., Makino K., Miki T., Mizobuchi K., Mori H., Morimura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Moshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-0157:H7 / EDE933 / ATCC 700927;

MEDLINE-21074935; PubMed-11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              corresponding to the 28.0-40.1 min region on the linkage map."; DNA Res. 3:363-377(1996).
                            7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                    I -> V (IN RNA EDITED VERSION). /FTId=VAR_010168.
                                                                                                    /FIId=VAR_003450.

I -> V (IN RNA EDITED VERSION).
/FIId=VAR_010166.
N -> S (IN RNA EDITED VERSION).
/FIId=VAR_010167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            famamoto Y., Horiuchi T.;
"A 570-kb DNA seguence of the Escherichia coli K-12 genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                    12.6%; Score 67; DB 1; Length 458;
                                                                                                                                                                                                                                                                                  29; Indels
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                      9E76B3FFD3E09C93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 AA
                                                                           BY SIMILARITY.
                                                                                                                                                                                                                                                                     Local Similarity 27.4%; Pred. No. 5.4; hes 23; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     329 ITNIL--SVLC----EKSCNQKL 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein ynf1 precursor.
YNF1 OR B1591 OR 22581 OR ECS2297.
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                                                                                                                                                                                                                         458 AA; 51821 MW;
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                                                                                                                                                         158
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333
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Mau B., Shao Y.;
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P76174; P77270;
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                                 TRANSMEM
                                                               CARBOHYD
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   TRANSMEM
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                                                                                                                                                                SECORDE FROM N.T.

STRAIN=0157H PARIND 0509952;

MEDLINE=21156231; PubMed=11258796;

MEDLINE=21156231; PubMed=11258796;

MEDLINE=21156231; PubMed=11258796;

MEDLINE=21156231; PubMed=11258796;

Hayashin T., Makino K., Ohnishi M., Turokawa K., Tanaka M., Tobe T.,

Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli

0157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res 8: 8:11-22(201).

--- SIMILARITY: TO H.INFLENZAE HI1044.

--- SIMILARITY: BELONGS TO THE YCDY/YNFI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vicia sativa (Spring vetch) (Tare).

Vicia sativa (Spring vetch) (Tare).

Eukaryota; Viridiplantes, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; Spermatophyta; Rabales; Rabaceae, Papilionoideae; Vicieae; Vicia.
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BEDINRE-98264856; PubMed-9601090;
Tijet N., Helvig C., Pinot F., Le Bouquin R., Lesot A., Durst F., Salauen J.-P., Benveniste I.;
                                                                                "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cytochrome P450 94A1 (EC 1.14...) (P450-dependent fatty acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.3%; Score 65.5; DB 1; Length 207; 28.7%; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL PROTEIN YNFI. 458DDBF76D16EA89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Signal; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 28.7%; Pred. No. 3.4;
nes 25; Conservative 14; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 SLLCPPSPKEVTCREMLTGGCLPWATR 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, D90801, BAA15315.1; ALT_INIT.
EMBL, D90802, BAA15325.1; ALT_INIT.
EMBL, AE005382, AAG56578.1;
ECBL, AF002557; BAB35720.1;
ECOGENE: EG13847; ynfi
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                                                                                                            Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A.
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CYP94A1 OR VAGH111.
                                                                                                                                                       SEQUENCE FROM N.A.
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O81117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306 ADIVISFILAGKDTTSAALTWFFWLLWKNPRVEEEIVNELSKKSELMVYDEVKEMVYTHA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 RDHASLGDSETLSQ--TELR----KKERKKKRE------------RKFQ 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----LFSHH 57
                                                                             "Functional expression in yeast and characterization of a clofibrate-inducible plant cytochrome P-450 (CYP94A1) involved in cutin monomers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P79960; P70058;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
G protein-coupled receptor APJ homolog (Angiotensin receptor related protein) (Mesenchyme-associated serpentine receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Devic E., Paquereau L., Vernier P., Knibiehler B., Audigier Y.; "Expression of a new G protein-coupled receptor X-msr is associated with an endothelial lineage in Xenopus laevis."; Mech. Dev. 59:129-140(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      366 ALSESMRLYPPVPMD--SKEAVNDDVLPDGWVVKKGTIVTYHVYAMGRMK 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 WIQESL-LCPPSPKEVTCREMLTGGCLP--WATRS-----HLGRRK 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.2%; Score 65; DB 1; Length 514; 20.0%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33; Indels
                                                                                                                                                                                                                                                                                      similarity).
-1- INDCTION: By clofibrate.
-1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             458 458 HEME (BY SIMILARITY).
514 AA; 59110 MW; 3D9361380D6C3B0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 ANCGIDFI-----IFWIFWIL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          353 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF030260; AAD10204.1; -. InterPro; IPR001128; Cytochrome_P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevīs (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97109511; PubMed=8951791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8355;
                                                              synthesis.
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REPRESENTATION OF THE PROPERTY OF THE PROPERTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                    in the mesodermal layer and at the neurula stage, exclusively expressed in the mesodermal layer and at the neurula stage in the lateral plate mesoderm. Larval expression is observed in the endothelium of the primary blood vessels and the forming heart.

-I- DEVELOPMENTAL STAGE: First expressed at the late blastula stage, increases during gastrulation and remains constant between neurula
                                                                                                                                         -1- FUNCTION: Putative receptor for an apelin-like peptide coupled to G proteins that inhibit adenylate cyclase activity.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                           and larva stages.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                          Saha M.S., Oakes J.A., Miles R.R.;
"XAngiol, a novel Xenopus gene, is expressed in vascular precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLONAC. .) (POTENTIAL).
N-LINKED (GLONAC. .) (POTENTIAL).
P -> S (IN REP. 2).
1BF757D865057621 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X93045; CARLOULL; -
EMBL; U72029; AAB17004.1; -
InterPro; IPR000276; GPCR_Rhodpsn.
PROWITS; PR00037; GPCRRHODDSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G_PROTEIT; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G_PROTEIT COULDED FINANCIAL TRANSMEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.8%; Score 63; DB 1; Length 353; 30.6%; Pred. No. 11;
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                           Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22; Indels
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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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01-JAN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ATP synthase delta chain (EC 3.6.3.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Pred. No. 11;
12; Mismatches
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SEQUENCE OF 1-303 FROM N.A.
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Matches 15; Conservative
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72
95
109
131
150
173
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19
181
150
353 AA;
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151
174
207
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ATPD_VIBAL
SOLUTION OF THE STAND STAND STAND SOLUTION OF THE STAND STAND STAND SOLUTION OF THE STAN
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TRHY_SHEEP
P22793;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed-10984043;
Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E., W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                  CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL, CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C. SIMILARITY: BELONGS TO THE ATPASE DELTA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09HWR3.
16-007-2001 (Rel. 40, Last sequence update)
16-007-2001 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable bacteriophytochrome (EC 2.7.3.-) (Phytochrome-like protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                              SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
                                                                                          MEDINE=90016889; PubMed=2529481;
Krumholz L.R., Esser U., Simoni R.D.;
Krumholz L.R., Esser U., Simoni R.D.;
"Nucleotide sequence of the unc operan of Vibrio alginolyticus.";
"Nucleic Acids Res. 17:7994 (1989).
-!- FUNCTION: THIS PROTEIN SEEMS TO BE PART OF THE STALK THAT LINKS
CF(0) TO CF(1). IT EITHER TRANSMITS CONFORMATIONAL CHANGES FROM
CF(0) INTO CF(1) OR IS IMPLICATED IN PROTON CONDUCTION.
-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 VSRDHASLGDSETLSQTELRKKE------RKKKRERKFQANCGID 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIMYS; PRO0125; ATPASEDELTA.
TIGREAMS; TIGRO1145; ATP_Synt_delta; 1.
PROSITE; PSO0389; ATPASE_DELTA; 1.
Hydrolase; ATP synthesis; CF(1); Hydrogen ion transport.
SEQUENCE 177 AA; 19489 MW; E8A311993DA63E4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.7%; Score 62.5; DI 30.4%; Pred. No. 6.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 728 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP, P00831; 1ABV.
InterPro; IPR000711; ATPSynt_OSCP.
Pfam; PF00213; OSCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X16050; CAA34178.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 30.4% nes 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         opportunistic pathogen."; Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S06079; S06079.
                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BPHP OR PA4117
          NCBI_TaxID=663;
                                                                                                                                                                                                                                                                                               H(+)(Out).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BPHY_PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
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          δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 GDSETLSQTELRKKERKKKRERKFQAN-------CGIDFIIF-----WIFWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HISTIDINE KINASE.

CHROMOPHORE (POTENTIAL).

PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

80930 MW; EEE9259392E5C4B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32; Indels 39; Gaps
                                                                                                                                                                 SIMILARITY).
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE PHYTOCHROME
                                    REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE R FORM THAT ABSORBS MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE FR FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ovis aries (Sheep).
Subaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidea; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             427 --FRHEEVHRIRWGGKPEKLLTIGPSGPRLTPRGSFEAWEEVVRGHSTPWS 475
                                FORM THAT ABSORBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 LLFSHHWI-----QESLLCPPSPKEVTCR-----EMLTGGCLPWA 86
-! - FUNCTION: PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sensory transduction; Transferase; Kinase; Phosphorylation; Photoreceptor; Phytochrome; Chromophore; Complete proteome. DOMAIN 17 495 CHROMOPHORE BINDING DOMAIN.
                                                                                                                                                                                                                                                          -!- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pfam; PF00360; phytochrome; 1.
Pfam; PF00360; phytochrome; 1.
Pfam; PF00512; signal; 1.
Pfam; PF01590; GAF; 1.
Pfam; PF01599; GAF; 1.
PRINTS; PR00344; BCTRLSENSOR.
PRINTS; PR00344; BCTRLSENSOR.
SWART; SW00065; GAF; 1.
SWART; SW00388; Hisral.
SWART; SW00388; Hisral.
PROSITE; PS50109; HIS.
PROSITE; PS501046; PHYTOCHROME_1; FALSE_NEG.
PROSITE; PS50046; PHYTOCHROME_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1991 (Rel. 19, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.7%; Score 62.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HESP; P02933; 1JOY.
INTERPO: PRR003594; ATPDING_ATPASE.
INTERPO: IPR003598; Bact_sens_pr_C.
INTERPO: IPR003018; GAF.
INTERPO: IPR004359; HIS.KIN_sig.
INTERPO: IPR0043594; HIS.KINA.
INTERPO: IPR001294; Phytochrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE004828; AAG07504.1; -.
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Best Local Similarity 23.4%
Matches 26; Conservative
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728 AA;
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REM 1119

REM SEROUGUE FROM N.A.

REM STATES—925 COLOUGH PURMED—7084001;

REM STATES—925 COLOUGH PURMED—7084001;

REM STATES—13. MCELOMIAID C.J.; Compbell M.T., Rogers G.E.;

REM STATES—925 COLOUGH PURMED—13. MCELOMIAID IN THE NAIT FOLICIS.

REM STATES—13. MCELOMIAID C.J.; Compbell M.T., Rogers G.E.;

REM STATES—13. MCELOMIAID C.J.; COMPBELL MCELORITHMS AND STATES—13. COLOURS—13. MCELOMIAID C.J.; COLOURS—13. MCGLOMIAID C.J.; COLOURS—13. MCGLOMIAID C.J.; COLOURS—13. M
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15-JUN-2002 (Rel. 41, Last annotation update)
Putative acyl carrier protein phosphodiesterase 1 (EC 3.1.4.14) (ACP
                                                                                                  AA APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=13 / Type A;
PubMed=11792842;
Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
Shiba T., Oqasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
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                                                                                                                        2-4.

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1122
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18.
MISSING (IN SHORT FORM).
E > G (IN REF. 2).
MY: E72FB9FF1326E54E CRC64;
Score 62; DB 1; Length red. Nismatcher
                                                                                                                                                                                                                                                                                                                         DB 1; Length 1549;
                                                                                                                                                                                                                                                                                                                                                              1 EVEVSRDHASLGDSETLSQTELRKKERKKKRERKF 35
                                                                                                 23 X 23 Z
                                                            1-10.
                                                                            1-12.
1-13.
1-14.
  1-2.
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1-5.
1-5.
1-8.
                                                                                                                                                                                                                                                                                                                                                                                               ACD1_CLOPE
ID ACD1_CLOPE STANDARD; E
AC Q8XMZ.
DT 15-UJN-2002 (Rel. 41, Created)
DT 15-UJN-2002 (Rel. 41, Last sequ
                Clostridium perfringens
                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphodiesterase 1).
                                                                                                                                                                                                                                                                                                                             Local Similarity
tes 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     flesh-eater.";
                                                                                                                                                                                                                                                                                        VARIANT
CONFLICT
                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                        REPEAT
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REPEAT
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                                                                                                 DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 EVDLYKDFIPRLEHKHFSGRSSVVDCETASIDAKTKEEVKRIIELSEQFKNADLYVIAAP 100
                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVEVSRD-------HASLGDSETLSQTELRKKERKKKRERKFQANCGIDFIIFWI 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Erdmann J., Nothen M.M., Shimron-Abarbanell D., Rietschel M., Albus M., Borrmann M., Maier W., Franzek E., Korner J., Weigelt B., Finmers R., Propping P.;
"The human serotonin 7 (5-HT7) receptor gene: genomic organization and systematic mutation screening in schizophrenia and bipolar affective disorder.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5HT. HUMAN STANDARD; PKRI; 4/2 AA.
P34969; P78516; P78336; P78372;
O1-FEB-1994 (Rel. 28, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
5-hydroxytryptamine 7 receptor (5-HI-7) (5-HT-X) (Serotonin receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
MEDLINE=97238071; PubMed=9084407;
Heidmann D.E.A., Metcalf M.A., Kohen R., Hamblin M.W.;
Heidmann D.E.A., Metcalf M.A., Kohen R., Hamblin M.W.;
Frout 5-hydroxytryptamine7 (5-HT7) receptor isoforms in human and rat produced by alternative splicing: species differences due to altered intron-exon organization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 FWILLFSHHW-----IQESLLCPPSPKEV-----TCREML----TGGCLPWATR 88
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bard J.A., Zgombick J.M., Adham N., Vaysse P., Branchek T.A., Weinshank R.L.; "Cloning of a novel human serotonin receptor (5-HT7) positively
                                                                                                                                                                                                                                                                                                                                                                                     29;
                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 218;
                                                                                                                                                                                                                                                                                                                                                                                       42; Indels
                                                                                                                                                                                                                                                                                           Hypothetical protein; Hydrolase; Complete proteome. SEQUENCE 218 AA; 24965 MW; 82E54E1A03EE253F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                  Score 61.5;
                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biol. Chem. 268:23422-23426(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM A).
TISSUE-Placenta, and Fetal brain;
MEDLINE-94043137; Pubmed-8226867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neurochem. 68:1372-1381(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97298817; PubMed=9154233;
                                                                                                                                                                                                                                                                          EMBL; AP003187; BAB80262.1; -.
                                                                                                                                                                                                                                                                                                                                                  11.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linked to adenylate cyclase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Psych. 1:392-397(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANTS LYS-92 AND LEU-279
                                                                                                                                                                                                                                                                                                                                                                    24.8%;
                                                                                                                                                                                                                                                                                                                                                                                       29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PALMITATE (POTENTIAL).
MISSING (IN ISOPORM B).
RACTRAVLIAPEKREPVSVWVLQSPOHHNWLADKMLTTVEK
KVMIHD -> QNADYCRKKGHDS (IN ISOFORM A).
                                                                    -1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: D (SHOWN HERE), A AND B; ARE PRODUCED BY ALTERNATIVE SPLICING. ISOFORM D IS THE LONGEST ISOFORM BUT ISOFORMS A AND B APPEAR TO BE EXPRESSED AT HIGHER LEVELS.
-1- TISSUE SPECIFICITY: ISOFORM A IS THE PREDOMINANT ISOFORM IN SPLEEN, CADDATE AND HIPPOCAMPUS. ISOFORM B IS EXPRESSED AT LOWER LEVELS, AND ISOFORM D IS A MINOR ISOFORM.
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTIONS AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATE ADENYLATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 POTENTIAL. (POTENTIAL). CYTOPLASMIC (POTENTIAL). N-LINKED (GLCNAC. . .) (POTENTIAL). N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000276; GPCR_Rhodpsn.
PRIMTS, PR00237; GPRERHODDSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00252; G_PROTEIN_RECEP_F1_2; 1.
G_protein coupled receptor; Transmembrane; Glycoprotein;
Multigene family; Lipoprotein; Palmitate; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 61.5; DB 1; Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTId=VAR_012996.
1F62E985EADE1F23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 POTENTIAL.
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EMBL, U68492, AAF07217.1, JOINED.
EMBL, U68493, AA548397.2, -..
EMBL, U68492, AA848397.2, -..
EMBL, L21195, AA648397.2, JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  479 AA; 53554 MW;
                                                                                                                                                                                                                                                                                                            EMBL; U68487; AAB48393.1; -. EMBL; U68488; AAB48394.1; -. EMBL; U68492; AAF07218.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83
104
1104
1117
1138
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1222
222
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479
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"Cloning and characterization of a gene from Rhizobium melilotii 2011 coding for ribosomal protein Si.";
Nucleic Acids Res. 16:3075-3089(1988).
                                                                                                                                                                                                                                                                                                       01-JAN-1990 (Rel. 13, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
30S ribosomal protein S1.
RPSA OR R00255 OR SMC00335.
Rhizobium mellioti (Sinorhizobium mellioti).
Bacteria: Proteobacteria: alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP, P05055, 1SRO.
InterPro: IPR00110; Ribosomal_S1.
InterPro: IPR00110; Ribosomal_S1.
Ffam: PR0075, S1; 6.
PRINTS: PR00681; RIBOSOMALS1.
SWART; SW00316; S1; 6.
IGREPAMS: IIGREPAMS: ISPSA; 1.
PROSITE; PS50126; S1; 6.
Ribosomal protein; Repeat; RNA_binding; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=RCR2011 / SU47;
MEDLINE-88217521; PubMed=3368316;
Schhaer J., Thamm S., Lurz R., Hussain A., Faist G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOTIF 1.
MOTIF 2.
MOTIF 3.
MOTIF 4.
                                                                                                                               --TARPFICGISCSCIPLWVERIFL 370
                                                                           71 EVTCREMLTG---GCLP-WATRSHL 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21396507; PubMed=11481430;
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PIR; S01055; R3ZR1.
                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dobrinski B.
                                                                                                                                                                                                                                                              RS1_RHIME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLG_HRV89 STANDARD; PRT; 2164 AA. POLG_HRV89 STANDARD; Q82098; Q82099; Q82100; Q82101; Q820102; Q820104; Q82104; Q82105; Q820105; Q82104; Q82105; Q82104; Q82105; Q82106; Q82
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Duechler M., Skern T., Sommergruber W., Neubauer C., Gruendler P., Fogy I., Blaas D., Kuechler E.; Fogy I., Blaas D., Kuechler E.; Fogy I., Blaas D., Kuechler E.; Fuchler E.; Fuchler E.; Fogy I., Blass D., Kuechler E.; Fuchler E.; Fogy I., Blass B., St. 12605-2609(1987).

Froc. Natl. Acad. Sci. U.S.A. 84:2605-2609(1987).

FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN Q/G SITES IN THE POLYPROTEIN. IT MAX BE A CYSTEINE PROTEASE.

-!- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN O/G SITES IN THE POLYPROTEIN. IT MAX BE A CYSTEINE PROTEASE.

-!- CATALYTIC ACID TO THE POLYPROTEIN. IN Other picornavirus reactions Glu may substituted for Gln, and Ser or Thr for Gly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            {RNA)(N).
SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
                                                              -> ADAOPAALRN (IN REF. 1).
                                                                                                                                                                                                                                                                                                ij
                                                                                                                                                                                                                                        DB 1; Length 568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
                                                                                                                                                                                                                                                                                                                                                                                 1 EVEVSRDHASLGDSETLSQTELRKKERKKKRERKFQANCGIDFIIF 46
                                                                                                                                                                                                                                                                                          12; Mismatches 16; Indels
S1 MOTIF 6.

A -> R (IN REF. 1).

LHINDQPEI -> ADAQFAALRN (IN P. K (IN REF. 1).

L -> Q (IN REF. 1).

A -> R (IN REF. 1).

A -> R (IN REF. 1).

W; ABO858204273A7B8 CRC64;
                                                                                                                                                                                                                                                                   Pred. No. 27;
                                                                                                                                                                                                                                     11.6%; Score 61.5;
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InterPro; IPR0002527; Pico_P2B.
InterPro; IPR000605; RNA_helicase.
InterPro; IPR001205; RNA_pol_P3D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=87204179; PubMed=3033653;
                                                                                                                                                                         62640 MW;
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Pico_P2A.
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EMBL; A10937; CAA00931.1; -.
PIR; A29862; GNNY89.
                                                                                                                                                                                                                                                             Local Similarity 37.0%
nes 17; Conservative
  530
88
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235
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551
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InterPro; IPR003138;
                                                                                                              241
551
568 AA;
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                                                        CONFLICT
                                                                                                                                              CONFLICT
                                CONFLICT
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                                                                                                                 CONFLICT
     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid pSRQ11, and Plasmid pSMB74.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae; Pediococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=PAC-1.0; PLASMID=PSRQ11;
MEDLINE=92384551; PubMed=1514784;
MEDLINE=92384551; PubMed=1514784;
Marugg J.D., Gonzalez C.F., Kunka B.S., Ledeboer A.M., Pucci M.J.,
Toonen M.Y., Walker S.A., Zoetmulder L.C.M., Vandenbergh P.A.;
"Cloning, expression, and nucleotide sequence of genes involved in
production of pediocin PA-1, and bacteriocin from Pediococcus
acidilactici PAC1.0.";
Appl. Environ. Microbiol. 58:2360-2367(1992).
                                                                                                                                                                                            Thiol protease; Myristate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=H; PLASMID=pSMB74;
MEDLINE=94288967; PubMed=7764941;
Motlagh A.M., Bukhtiyarova M.B., Ray B.R.;
Complete nucleotide sequence of pSMB 74, a plasmid encoding the production of pediocin AcH in Pediococcus acidilactici.";
Lett. Appl. Microbiol. 18:305-312(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 61.5; DB 1; Length 2164;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                          GENOME-LINKED PROTEIN VPG (P3B).
                                                                                                                                                                                                                                                                                                                                                                          RNA-DIRECTED RNA POLYMERASE P3D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      PROTEASE (POTENTIAL).
PROTEASE (POTENTIAL).
W: F5D9C8F4FBEA7D54 CRC64;
                                                                                                                     Probom; PD001125; Cys-protease-3C; 1.
Probom; PD001274; Pico_P2B; 1.
Probom; PD001274; Pico_P2B; 1.
Probom; PD001276; Pico_P2B; 1.
Polyprotein; Coat protein; Transferase; RNA-directed RNA polymerase; Hydrolase; Thiol protease; CHAIN 37 574 COAT PROTEIN VP2 (PIB). CHAIN 875 866 COAT PROTEIN VP3 (PID). CHAIN 867 1008 CORE PROTEIN VP3 (PID). CHAIN 1009 1103 CORE PROTEIN P2B. CHAIN 1104 1424 CORE PROTEIN P2C. CHAIN 1425 1500 CORE PROTEIN P3A.
                                                                                                                                                                                                                                                                                                                                                                                         MYRISTATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPA1_PPEDAC STANDARD; PRT; 62 AA. P29430; P39430; P394312; 01-APR-1993 (Rel. 25, Created) Ol-JUN-1994 (Rel. 29, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Bactericcin pediccin PA-1 precursor (Pediccin ACH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Mismatches
                                                                                                                                                                                                                                                                                                                                                           PICORNAIN 3C.
                            Pfam; PF00548; Cys-protease-3C; 1. Pfam; PF00680; RNA_dep_RNA_pol; 1. Pfam; PF00910; RNA_helicase; 1. Pfam; PF00947; Picc_P2A; 1. Pfam; PP01552; Picc_P2B; 1. Pfam; PF02226; Picc_P1A; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24; Conservative
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1668
1682
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2164 AA;
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Best Local Similarity
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                        Gen. Microbiol. 138:1985-1990(1992).
- FUNCTION: BACTERICIDAL ACTIVITY (EFFECTIVE INHIBITOR OF LISTERIA
MONOCYTOGENES).
                                                                                                                                                MEDLINE-93019000; PubMed-1402795; Cazano J.C.N., Meyer J.N., Sletten K., Pelaz C., Nes I.F.; Purification and amino acid sequence of a bacteriocin produced by Pediococous acidilactici.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                           STRAIN=PAC-1.0; PLASMID=PSRQ11;
MEDLINE=92246549; PubMed=1575516;
Henderson J.T., Chopko A.L., van Wassenaar P.D.;
Purification and primary structure of pediocin PA-1 produced by Pediococcus acidilactici PAC-1.0.";
Arch. Biochem. Biophys. 295:5-12(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                         SUBCELLULAR LÓCATION: Secreted.
SIMILARITY: BELONGS TO BACTERIOCIN CLASS IIA/YGNGV FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
SEQUENCE FROM N.A.
MEDLINE-89042086; PubMed-2847145;
Watson D.K., McWilliams M.J., Lapis P., Lautenberger J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 61; DB 1; Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BACTERIOCIN PEDIOCIN PA-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6644 MW; 8E6F10D49FA87BA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYDROPHOBIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 KEVICREMLIGGCLPWAIRSHLGRRKC 96
[3]
SEQUENCE OF 19-62, AND DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002633; Bacteriocin_II. Pfam; PF01721; Bacteriocin_II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01721; Bacteriocin_II; 1. ProDom; PD004452; Bacteriocin_II; 1. Antibiotic; Bacteriocin; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M83924; AAA25559.1; -. EMBL; M90679; AAA98337.1; -. EMBL; U02482; AAC43293.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A41823; A41823.
PIR; S21699; S21699.
PIR; A48941; A48941.
PIR; A47680; A47680.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1990 (Rel. 14, 01-APR-1990 (Rel. 14, 16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      musculus (Mouse).
                                                                                                                                    SEQUENCE OF 19-61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C-ETS-2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P34034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETS2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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ETS2_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 KENQEKTEDOYEENSHLNAVPHWINSNTLGFSMEQAPYGMQAPNYPKD----NLLDSMCP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 KERKKKRERKFQANCGIDFIIFWIEWILL-FSHHWIQESLLCPPSPKEVTCREMLTGGCL 83
                          "Mammalian ets-1 and ets-2 genes encode highly conserved proteins.";
Proc. Natl. Acad. Sci. U.S.A. 85:7862-7866(1988).
-!- SUBCELLUIAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE ETS FAMILY.
-!- SIMILARITY: CONTAINS 1 POINTED (PNT) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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"The nucleotide sequence and genome organization of human papilloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 11.4%; Score 60.5; DB 1; Length 4 1 Similarity 29.0%; Pred. No. 29; 20; Conservative 12; Mismatches 32; Indels
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5260F3085B7EB831 CRC64;
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PROSITE; PS00346; ETS_DÓMAIN_2; 1.
PROSITE; PS50061; ETS_DOMAIN_3; 1.
DOMAIN 87 170 POINTED.
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23-00T-1986 (Rel. 02, Last sequence update)
01-AUG-1990 (Rel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP, P4921; 2STT.

TRANSFA: T01397;

MGD; MG1:95456; Ets2.
InterPro: IPR00241; HSF_ETS.
InterPro: IPR002341; HSF_ETS.
InterPro: IPR003118; SAM_PNT.
Pfam; PF00178; Ets; 1.
Pfam; PF02198; SAM_PNT; 1.
Pfam; PR0444; ETSOMAIN.
SNART; SM00413; ETS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  468 AA; 52827 MW;
Schweinfest C.W., Papas T.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; J04103; AAA37581.1; -. PIR; C32066; TVMSE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virology 151:124-130(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 PSATPAALG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 PWATRSHLG 92
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Best Local Similarity
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P04016;
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SEQUENCE
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RETARENT SET TENT SET
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9, 2003, 15:05:28; Search time 43.7788 Seconds (without alignments) 456.536 Million cell updates/sec
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532
1 EVEVSRDHASLGDSETLSQT......LTGGCLPWATRSHLGRRKCS
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                       671580 seqs, 206047115 residues
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Listing first 45 summaries
                                                                                  - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                          Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                       Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_virus:*
sp_vertebrate:*
sp_unclassified:*

sp_rodent:* sp_plant:*

sp_rvirus:*
sp_bacteriap:*
sp_archeap:*

sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_nammal:*
sp_mammal:*

sp_organelle:* sp_phage:*

ŭ		Description	O96ex2 homo sapien	Q9knh2 vibrio chol	Q9m896 arabidopsis	O11498 human immun	O11503 human immun	O11505 human immun	Q9u0q5 plasmodium	016652 caenorhabdi	011502 human immun	O11504 human immun	Q9yiw8 human immun	Q9epj7 mus musculu	Q8uqb2 human immun	Q9u418 branchiosto	Q18657 caenorhabdi	Q8uqa8 human immun
COMMARTED		ID	Q96EX2	Q9KNH2	968M6Q	011498	011503	011505	090005	016652	011502	011504	O9YIW8	<b>09EPJ7</b>	Q8UQB2	Q9U418	Q18657	Q8UQA8
		DB	4	16	10	15	15	15	2	Ŋ	15	15	15	11	15	Ŋ	Ŋ	15
		Query Match Length DB	231	177	373	396	396	368	2277	684	396	396	353	463	169	411	1851	169
	дP	Query Match	15.8	13.6	13.5	13.5	13.5	13.5	13.3	13.2	13.0	13.0	12.9	12.8	12.7	12.7	12.6	12.5
		Score	84	72.5	72	72	72	72	71	70	69	69	68.5	99	67.5	67.5	67	66.5
		Result No.	1	7	ო	4	2	9	7	œ	თ	10	11	12	13	14	15	16

096296 plasmodium	O9vd16 drosophila	061730 drosophila	Q9vrr0 drosophila	. Q8uqc1 human immun	Q8uqc9 human 1mmun	Q8uqd7 human immun			_	Q9w248 drosophila	Q8swq1 encephalito	Q8uqb5 human immun	093081 human 1mmun		Q944s6 arabidopsis	Q8s2t0 arabidopsis	Q9txp5 caenorhabdi	Q46472 chlorobium	Q94du0 oryza sativ	Q9y7e0 aspergillus	Q8uqb3 human immun	Q8uqb1 human immun	Q99j63 mus musculu		Q99p01 cricetulus	Q9p3u8 schizosacch	Q9wmu7 human immun	
5 096296	5 09VDJ6		α			15 Q8UQD7					Ø						5 Q9TXP5	α		ø	15 Q8UQB3		11 099J63			ø	15 Q9WMU7	ALIGNMENTS
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12.5	12.4	12.4	12.4	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.1	12.1	12.1	12.1	12.1	12.1	12.0	12.0	12.0	12.0	11.9	11.9	11.9	11.9	11.9	11.9	11.9	
66.5	99	99	99	65	65	65	65	65	65	65	64.5	64.5	64.5	64.5	64.5		64	64	64	64	Э.	Э.	63.5	ë.	۳,	ش	θ.	
17	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

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3 EVSRDHASLGD--SETLSQTEL-----RKKERKKKRERKFQANCGIDFI-1FWIFWIL 52
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
similar to hypothetical 20, Last annotation update)
similar to hypothetical protein FLJ14627.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidee; Homo.
                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                               15.8%; Score 84; DB 4; Length 231; 31.2%; Pred. No. 0.047; tive 16; Mismatches 18; Indels
                                                                                                                                                                                                                     Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011878; AAH11878.1; -.
InterPro: IPR000345; CytC_heme_bind.
PROSITE; PS00190; CYTCCHROME_C; UNKNOWN_1.
SEQUENCE 231 AA; 25722 MW; B4D36B0360D3C57C CRC64;
              231 AA
              PRT;
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 31.2%
Matches 20; Conservative
             PRELIMINARY;
                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
TISSUE-MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LFCH 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 LFSH 56
                                                                                                                                                         NCBI_TaxID=9606;
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                               Q96EX2;
             Q96EX2
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296EX2
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177 AA.

PRT;

PRELIMINARY;

Q9KNH2;

Q9KNH2

Q9KNH2 ID Q9 AC Q9

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5 SRDHASLGDSETLSQTELRKKERKKKRERKFQANCGIDFIIFWIFWILLFSHHWIQESLL 64

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                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN-EL TOR N16961 / SERCTYPE 01;

MEDLINE-20406683; Pubmed-10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vannathevan J., Bass S., Oin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRAIN—CV. COLUMBIA,
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
Ronning C.M., Koo H., Fujii C.Y., Utterbock T.R., Barnstead M.E.,
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC F16B3 genomic sequence.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AC021640; AAF72451.1;
-InterPro; IPR004253; DUF231.
Pfam; PF03005; DUF231; I.
SEQUENCE 373 AA; 43367 MW; 76DF8859CBF950A8 CRC64;
                                                                                                              Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                            DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 13.6%; Score 72.5; DB 16; Length 177; Similarity 32.6%; Pred. No. 0.87; 15; Conservative 11; Mismatches 13; Indels 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.5%; Score 72; DB 10; Length 373; Ilarity 30.3%; Pred. No. 2; Conservative 7; Mismatches 18; Indels 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 AA; 19558 MW; 218356C3B0937D52 CRC64;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    373 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00213; OSCP; 1.
PRINTS; PR00125; ATPASEDELTA.
TIGRFAMS; TIGR01145; ATP_Synt_delta; 1.
PROSITE; PS00389; ATPASE_DELTA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000711; ATPSynt_OSCP
                                                        ATP synthase F1, delta subunit. VC2767.
                                                                                                                                                                                                                                                                                                                                                                               Nature 406:477-483(2000).
EMBL; AE004342; AAF95906.1; -.
HSSP; P00831; 1ABV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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Best Local Similarity
Matches 23; Conserv
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SEQUENCE 177 AA;
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                                                                                           Vibrio cholerae.
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                                                                                                                             NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGR; VC2767;
                                                                                                                                                                                                                                                                                                                                                                  cholerae."
                                                                                                                Bacteria;
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Q9M896;
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260 YCNTTQLFNSTWNVTEGLNNTEGNDTIILPCRIKQIINMWQEVGKAMYAPPISGQIRCSS 319
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                                                                                                                                                                                                                                                                                                                                                                                                                            Balotta C., Riva C., Violin M., Colombo C., Galli M., Moroni M.; Analysis of the VI-V5 env region in Long-Term Non Progressor and in a rapid progressor infected individuals."; Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases. EMBL; UG95406; AAB52752.1; -. InterPro; IPRO00777; GP120. Pfam; PF00516; GP120; 1.
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                      48;
                                                                                                                                                                                                                                                                                                                            13.5%; Score 72; DB 15; Length 396; 20.2%; Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                                                                      32; Indels
                                                                                                                                                                                                                                                                                                    396 AA; 44103 MW; 457EC5D0CA1A9E54 CRC64;
                                             01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                             Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
                          396 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    396 AA
                                                                                                                                                                                                                                                                                                                                                     19; Mismatches
                                                                                      Envelope glycoprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Envelope glycoprotein (Fragment).
                                                                                                                                                                                                                                                                Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                        Local Similarity 20.29
                          PRELIMINARY;
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                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                     NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    320 NITG 323
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NON_TER
SEQUENCE
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                        011498
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RESULT 4
011498
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Gaps

28;

Indels

18;

7; Mismatches

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202 DIRQAHCSLGRAEWNNTLKQIVIKLKEQFKNKTIVFKQSSGGDPEIVMHSFNCGGEF--F 259
                                                                                                                                                                                                             3 EVSRDHASLGDSE---TLSQTELRKKERKKRERKFQA------NCGIDFIIF 46
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                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Balotta C., Riva C., Violin M., Colombo C., Galli M., Moroni M.;

Balotta C., Riva C., Violin M., Colombo C., Galli M., Moroni M.;

Analysis of the VI-V5 env region in Long-Term Non Progressor and in a rapid progressor infected individuals.";

Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.

EMBL, 195408; AAB52754.1;

Interpro; IPR000777; G9120.

Pfam; PF00516; GP120; 1.

AIDS: Coat protein; Glycoprotein.
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                                                                                                                                                 48; Gaps
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                                                                                                  DB 15; Length 396;
                                                                                                                      ; Pred. No. 2.2;
19; Mismatches 32; Indels
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396 AA; 44120 MW; EF6AD3F0B027FB21 CRC64;
                                      396 396
396 AA; 44050 MW; 1F7EC53DB27A8669 CRC64;
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Last annotation update)
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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                                                                                                      13.5%; Score 72; 20.2%; Pred. No.
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  AIDS; Coat protein; Glycoprotein
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
Var, MAL4P2.58
                                                                                                                           Best Local Similarity 20.29
Matches 25; Conservative
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22 LRKK--ERKKKRERKFQANCGIDFIIFWIFWILLFSHHWIQESLL-CPPSPKEVTCREML 78
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Culson A.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Culson A.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lighthing J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Philerry Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Eukaryota, Metazoa; Nematoda, Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                     Devlin K., Bowman S., Churcher C., Harris B., Harris D., Lawson D., Quail M., Barrell B.; Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases. EMBL. AL035475; CAB628891. -InterPro; IPR004258; PFEMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
MALAP2.58, VAR.
Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.3%; Score 71; DB 5; Length 2277; 23.9%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterston R.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF016673; AAB66123.1; ..
Interprevo; IPR00718; Peptidase_M13.
Pfam; PF01431; Peptidase_M13; 1.
SEQUENCE 684 AA; 79176 MW; C2A8C605CB007A08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                     Pfan; PF03011; PFEMP; 2.
SEQUENCE 2277 AA; 256122 MW; E4262CCA69DDEF93 CRC64;
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Last annotation update)
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MEDLINE-94150718; PubMed-7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TrEMBLrel. 05,
01-JUN-2002 (TrEMBLrel. 21,
T06D4.4 protein.
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Le T.T., Goela D.;
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                                                                                                                                                                                           STRAIN=3D7;
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"Analysis of the Vl-V5 env region in Long-Term Non Progressor and in a reapid progressor infected individuals.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U95405; AAB52751.1;
Interpro; IPR000777; Gp120.
Pfam: PF00516; Gp120;
AADS; Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
13.0%; Score 69; DB 15; Length 396;
Best Local Similarity 20.3%; Pred. No. 5;
Matches 25; Conservative 18; Mismatches 32; Indels 48; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Balotta C., Riva C., Violin M., Colombo C., Galli M., Moroni M.;
"Analysis of the VI-V5 env region in Long-Term Non Progressor and in a
rapid progressor infected individuals.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; 095407; AAB52753.1;
InterPro; IPR000777; GP120.
                                Gaps
                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                              DB 15; Length 396;
Ouery Match
Best Local Similarity 31.8%; Pred. No. 6.4;
Matches 14; Conservative 9; Mismatches 9; Indels
                            9; Indels
                                               23 RKKERKKKRERKFQA------NCGIDFIIFWIFWILLF 54
                                                                       8 KEKEKERKKAEKFSADEKTANIKDRIINCVYPVILIILFWLLLF 51
                                                                                                                                                                                                                                                                                                                                                                                              396 396
396 Aa; 43975 MW; FA685770CDCBCFE9 CRC64;
                                                                                                                                                          01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                      Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1997 (TrEMBLrel. 04, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Envelope 91ycoprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBL_TaxID=11676;
                                                                                                                                       PRT; 396 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1997 (TrEMBLrel. 04, Created)
                                                                                                                                                                                                Envelope glycoprotein (Fragment).
                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321 ITG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 LTG 80
                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
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                                                                                                           RESULT 9
011502
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260 YCNTTQLFNSTWNVTEGLNNTEGNDTIILPCRIKQIINMWQEVGKAMYAPPISGQIRCSS 319
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                                                                                                                                                                                                                                                                                                           3 EVSRDHASLGD---SETLSQTELRKKERKKRERKFQA------NCGIDFIIF 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTRAIN-UKRAINIAN;
Grebenjuk V.A., Anoprienko O.V., Skorokhod A.S., Marichev I.L.,
Kavsan V.M.;
Genetic characterization of HIV-1 variants in Ukraine [in Russian].";
Biopolymers & Call 14:277-285(1998).
EMBL; Y16082; CAA76048.1;
EMBL; Y16081; CAA76044.1;
InterPro: IPR000378; Env_GP41.
InterPro: IPR000378; GP120.
Pfam: PF00516; GP120.
Pfam: PF00517; GP120.
Pfam: PF00517; GP120.
Pfam: PF00517; GP120.
Pfam: PF00517; GP120.
Pfam: FF00517; GP120.
                                                                                                                               Query Match 13.0%; Score 69; DB 15; Length 396;
Best Local Similarity 19.4%; Pred. No. 5;
Matches 24; Conservative 20; Mismatches 32; Indels 48; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 12.9%; Score 68.5; DB 15; Length 353;
1 Similarity 19.2%; Pred. No. 5.1;
24; Conservative 19; Mismatches 33; Indels 49; Gaps
                                                                                      396 AA; 44074 MW; 281C76D80C080D1D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        353 353
353 AA; 39278 MW; BA670EBAC36227C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 10, Created)
(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       463 AA.
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Pfam; PF00516; GP120; 1.
AIDS: Coat protein; Glycoprotein.
NON_TER 1 1 1
NON_TER 36 396
SEQUENCE 396 AA; 44074 MW; 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENV protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         320 NITG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223 SNITG 227
                                                                                                                                                                                                                                                                                                                                                                                                 77 MLTG 80
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01-MAY-1999 (
01-OCT-2001 (
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NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9EPJ7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
Q9YIW8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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10 SLGDSETLSQTELRKKERKKKRERKFQANCGIDFIIFWI---FWILL-------
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-93USPIC1008EB3Y;
Muthui D., Brodie S.J., Learn G.H., Zhu T., Diem.K., Mullins J.I.,
                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                  46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Changes in the virus population in acute HIV-1 infection."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF418721; AAL72834.1; -.
Interpro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
                                                                                                                                                                                                                                                                                                                                                                        12.8%; Score 68; DB 11; Length 463; 22.8%; Pred. No. 7.6;
                                                                                                                                                                                                                                                                                                                                                                                                  41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 AA; 18687 MW; 271ABB2048D48A6F CRC64;
                                                                                                                                                                                                                                                                                                                                       463 463
463 AA; 52804 MW; BBC7E96FBB717CE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Glucocorticoid induced receptor (Fragment).
GPR83 OR GIR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Retroid viruses; Retroviridae; Lentivirus
                                                                                                                                                                                                                                                                          Pfam; PF00001; 7tm_1; 1.

PRINTS; PR00237; GPCRRHODPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 AA
                                                                                                                                                                                                                                                                                                                                                                                                 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Envelope glycoprotein gp120 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                      MEDLINE=20515601; PubMed=11060465;
                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 22.83
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : | | | | | | 445 KSH-GRR 450
                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RSHLGRR 94
                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=11676;
                                                                                                     NCBI_TaxID=10090;
                                                                                                                                            STRAIN-129SV;
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                              Receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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48 DIRKAHCNLTSTKWANTLSQIAKKLKEQSGNKTIVFNRSSGGDPEIVMHSFNCGGEF--F 105
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                                                            3 EVSRDHASLGDSE---TLSQTELRKKERKKRERKFQA------NCGIDFIIF 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         Yasui K., Saiga H., Uemura M., Semba I.;

A Yasui K., Saiga H., Uemura M., Semba I.;

Yasui K., Saiga H., Uemura M., Semba I.;

"Early body formation and expression pattern of genes encoding
T secreted proteins, BBBMP2/4, BBMR17, and BBMR18 in lancelets.";

L. Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

-:-SIMILARITY: BELONGS TO THE TGR-BETA FAMILY.

R HSSP; P12643; 3BMP.

R InterPro; IPR001839; TGP.

R InterPro; IPR001839; TGF.

R InterPro; IPR001111; TGF.

R Pfam; PF000689; TGF. beta; 1.

R Pfam; PR00669; INHIBINA.

R PRINTS; PR00669; INHIBINA.
                                                                                                                                          : ::: || ::| | ::| | 10.0 YCNTTQLFNSTWITPCRIKQIVNMWQEVGKAMYAPPIQGQITCSSNITG 158
                                                                                                                         Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
Branchiostoma.
                             37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23;
Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5; Length 411;
                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              411 AA; 46929 MW; F579898060F18355 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                  01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DB 15;
                               34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---VAPPGYQAYYCH----GEC-PFPLADHL 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.7%; Score 67.5; D
25.3%; Pred. No. 7.8;
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                                                                                                                                                                                                                                      411 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Mismatches
              ; Pred. No. 3.3; 19; Mismatches
12.7%; Score 67.5; 20.4%; Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
                                                                                                                                                                                                                                                                                                                                                   Branchiostoma belcheri (Amphoxius)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                  Bone morphogenetic protein 2/4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 25.33
Matches 23; Conservative
                               23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                      PRELIMINARY;
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                Best Local Similarity
Matches 23; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7741;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein
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   Query Match
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090418;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       018657
                                                                                                                                                                                                        RESULT 14
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NCBL_TaxID-6239;
RN | 11
RP SEQUENCE FROM N.A.
RA MCHULTAY A.A.;
LS Jubmitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
RN | 20
RN | 12|
RN | 13|
RN | 13|
RN | 14|
RN | 15|
RN |
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July 9, 2003, 15:05:28 ; Search time 8.92035 Seconds (without alignments) 239.005 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                               908470 seqs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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98
1 FQANCGIDFIIFWIFW 16
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Maximum DB seq length: 2000000000
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1. \CsiDS2/gcgdata/geneseqy/geneseqp-embl/AA1980_DAT:*
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3. \SiDS2/gcgdata/geneseqy-embl/AA1981_DAT:*
4: \SiDS2/gcgdata/geneseqy-embl/AA1981_DAT:*
4: \SiDS2/gcgdata/geneseqy-embl/AA1984_DAT:*
5: \SiDS2/gcgdata/geneseqy-embl/AA1984_DAT:*
6: \SiDS2/gcgdata/geneseqy-embl/AA1984_DAT:*
7: \SiDS2/gcgdata/geneseqy-embl/AA1986_DAT:*
8: \SiDS2/gcgdata/geneseqy-embl/AA1980_DAT:*
9: \SiDS2/gcgdata/geneseqy-embl/AA1980_DAT:*
10: \SiDS2/gcgdata/geneseqy-embl/AA1980_DAT:*
11: \SiDS2/gcgdata/geneseqy-embl/AA1980_DAT:*
12: \SiDS2/gcgdata/geneseqy-embl/AA1990_DAT:*
13: \SiDS2/gcgdata/geneseqy-embl/AA1991_DAT:*
14: \SiDS2/gcgdata/geneseqy-embl/AA1991_DAT:*
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16: \SiDS2/gcgdata/geneseqy-embl/AA1991_DAT:*
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20: \SiDS2/gcgdata/geneseqy-embl/AA1999_DAT:*
21: \SiDS2/gcgdata/geneseqy-embl/AA1999_DAT:*
22: \SiDS2/gcgdata/geneseqy-embl/AA1999_DAT:*
23: \SiDS2/gcgdata/geneseqy-embl/AA1999_DAT:*
23: \SiDS2/gcgdata/geneseqy-embl/AA1999_DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		h DB ID Description	22 AAE13851	H0001111111111111111111111111111111111	Z1 AA134083	21	20 AAW99067	20 AAWGGORG	000000000000000000000000000000000000000	250 TOWN 27	55	1 21 AAB57264 . Human prostate can	19	OF STANKE CC
		Match Length DB	16.	10	700	504	207	326	900	0.40	20	64	123	300
æ	Query	Match	100.0	21.0	0.10	51.0	48.0	48.0	0 0 7	0 1	46.9	46.9	46.9	C U
		Score	86	, R	5	20	47	47	77		46	46	46	7
	Result	No.	1		1	c	4	S	۷.	<b>&gt;</b> 1		æ	6	0

Human thoracic aor Human thoracic aor	human G-p	uman G-pro	G protein coupled	3-p	Human membrane or	RTA-like G protein	Drosophila melanod	Human polypeptide	Human polypeptide	Drosophila melanog	Human thyroid stim	iseď anti	a)	olvpept	Human stromal cell		٦		ene 43	la]	ed	Human colon cancer	an po	Helicobacter pylor	H. pylori GHPO 534	opa	>	$\circ$	_	ø	human sFv a	sFv a	human sfv a	
AAR48755 AAW02727	641	1472	7	722	47	334	22	m	17	271	43	33	394	9	19	AAW88495	2	20	398	319	537	3	019	591	844	579	375	739	537	AAW08501	50	0	AAW08505	
15	23	23	17	17	22	23	22	22	22	22	16	17	22	23	22	20	21	21	22	22	22	21	23	22	19	22	23	22	23	18	18	18	18	
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111	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

# ALIGNMENTS

AAE13851  AAE13851  AAE13851  AAE13851  AAE13851;  AAC  AAE13851;  AAC  AAE13851;  BAC  AAE13851;  AAC  AAC  AAC  AAC  AAC  AAC  AAC  A	.ide; 16 AA.	ry)	Human T cell epitope related to lung tumour-specific protein.	<pre>cein; immunostimulant; cytostatic; gene therapy; ine; immune response; lung cancer;</pre>	•			99991.	18037.	18937.	.517p.	14512.	18973.		Mohamath R, Secrist H, Benson DR, Indirias CY; SP, Algate PA, Elliot M, Mannion J, Kalos MD;
	AAE13851 ID AAE13851 standard; peptide; 16 AA. XX AC AAE13851;	26-FEB-2002 (first entry)	Human T cell epitope relat	<pre>Human; lung tumour protein; antisense-therapy; vaccine;</pre>	T cell epitope.	WO200172295-A2.	04-OCT-2001.	28-MAR-2001; 2001WO-US09991						(CORI-) CORIXA CORP.	Lodes MJ, n RA, Fling

us-09-854-133-587.rag

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RESULT 3
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                                                                                     The invention relates to isolated lung tumour-specific proteins and their corresponding cDNA molecules. Lung tumour-specific proteins and their antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer. The invention also relates to a composition useful for stimulating an immune response, and for treating cancer. The lung tumour specific oligonucleotide is useful in gene therapy and for diagnosis, detection and treatment of lung cancer. The present sequence is human T cell epitope related to lung tumour-specific protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Exopolysaccharide; EPS; ESP enzyme; EPS1; EPS2; EPS3; EPS4; EPS5; EPS6; EPS7; EPS8; EPS9; EPS10; EPS11; Lactobacillus helveticus strain LH59; activated D-galactose pyranose; saccharide; beta-glycosyltransferase; undecaprenyl-phosphate-glycosyl-t-phosphate-transferase; alpha-glycosyltransferase; EPS polymerase; glycosyltransferase; phosphofuranose; transporter; food; fermented milk product; yoghurt; cheese; flavour stability; organoleptic property.
                                                                                                                                                                                                                                                         Gaps
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m of}
                                New human lung-specific polynucleotides and polypeptides for the diagnosis and treatment of disease e.g. lung cancer - \,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant enzymes for synthesis of exopolysaccharides, particularly in lactic acid bacteria, for improving properti
                                                                                                                                                                                                                                  Length 16;
                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAZ45259, AAY54082, AAY54083, AAY54084; AAY54085
                                                                                                                                                                                                                                                                                                                                                                                                                                Enzyme EPS11 involved in exopolysaccharide biosynthesis.
                                                                                                                                                                                                                               100.0%; Score 98; DB 22;
100.0%; Pred. No. 1.1e-08;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 8; Page 130-131; 162pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Germond JE, Lamothe G;
                                                                                                                                                                                                                                                                                                                                                            AAY54085 standard; Protein; 504 AA.
                                                                  Claim 2; Page 378; 378pp; English
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98EP-0201311.
98EP-0201312.
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                                                                                                                                                                                                                                          Local Similarity 100.
Tes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lactobacillus helveticus,
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          WPI; 2001-639201/73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9962316-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                          27-MAR-2000
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                                                                                                                                                                                                           Seguence
                                                                                                                                                                                                                                                                                                                                                                                  AAY54085;
                                                                                                                                                                                                                               Query Match
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In a method to the synthesis of proyection of a certain of the certain of the certain of a certain of a certain of the certain of the certain of a certain of certain of certain of a certain of a certain of a certain of cert
exopolysaccharides (EPS). These enzymes are designated EPS1-EPS11, and are encoded by open reading frames eps1-eps11. The enzymes are isolated from Lactobacillus helveticus strain LH59. The proteins are used in a method for the synthesis of EPS, which includes at least one step
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 recombinant enzymes for biosynthesis of exopolysaccharides having antitumor or probiotic properties or useful in fermented milk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 8.6;
5; Mismatches.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY43787 standard; Protein; 504 AA.
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98EP-0201312.
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Best Local Similarity
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22-APR-1998;
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AAY4377-87 represent enzymes encoded by the eps operon of Lactobacillus helveticus LH59. The operon contains 11 open reading frames, and encodes enzymes (eps1. eps2, eps3, eps4, eps5, eps6, eps7, eps9, eps9, eps1. eps1. eps2, eps3, eps7, eps5, eps6, eps7, eps9, and eps11) that are involved in the biosynthesis of exopolysaccharides (EPS). The enzymes catalyse the formation of specific intersugar bonds. The enzymes catalyse the formation of specific intersugar bonds. The enzymes catalyse a process that includes at least one step of forming a bond (in alpha or beta anomeric form) between C1, carrying the reducing aldehyde group of an activated D-Galp (galactose in primer. The enzymes are used to produce EPS that have antitumor or primer. The enzymes are used to produce EPS that have antitumor or problotic properties or are used in foodstuffs to improve organoleptic qualities and flavour. When expressed by lactic acid bacteria, EPS impart a free-flowing character and/or a smooth, creamy texture to acidified milk products (yoghurt or cheese).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae; mraY; transferase; infection; pneumonia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reagents and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.0%; Score 50; DB 21; Length 504; 37.5%; Pred. No. 8.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lonetto MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW99067 standard; Protein; 207 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    meningitis; gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-134240/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              504 AA;
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Phospho-N-acetylmuramoyl-pentapeptide-transferase designated mray. Mray polynucleotides and proteins are useful for diagnosing susceptibility to diseases by detecting mutations or polymorphisms in the mray gene or analysing for the presence of amount of mray protein expressed in a The present sequence represents the ORF protein sequence of an isolated

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which can be used in treatment to enhance (agonist) or block (antegonist) or antisense sequence) max activity, therefore treating microbial diseases, especially Streptococcus pneumoniae diseases including outliss media, bacteraemia, conjunctivits, pneumonia, sinusitis, pleural empyema, endocarditis and especially meningitis. Epitopes of mray proteins and polynucleotides are useful immunogens (vaccines) for producing anti-mray antibodies for prevention of bacterial infections, and mray polynucleotides for prevention of bacterial infections, therapy) to prevent infections. Wray proteins, polynucleotides and their (ant)agonists can prevent and body implants to prevent bacterial
patient sample. Mray PCR probes are useful for diagnosing diseases, and can characterise the response of the infectious organism to drugs. Mray proteins and polynucleotides are also useful for screening for antaqonists, agonists and drugs against infectious micro-organisms. Mray agonists and antagonists are bacteriostatic and bacteriocidal compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae; mraY; transferase; infection; pneumonia; phospho-N-acetylmuramcyl-pentapeptide-transferase family; otitis media; bacteraemia; conjunctivitis; sinusitis; pleural empyema; endocarditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents an isolated Phospho-N-acetylmuramoyl-pentapeptide-transferase designated mraY. MraY polynucleotides and
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                   Score 47; DB 20; Length 207; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae mraY transferase.
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24 YQVHLGIFYIVFALFW 39
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97US-0055467.
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4atches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            meningitis; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang M;
                                                                                                                                                                                                                                                                                                                                207 AA;
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                                                                                                                                                                                                                                                                                              infection
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proteins are useful for diagnosing susceptibility to diseases by
detecting mutations or polymorphisms in the mray gene or analysing for
the presence of amount of mray protein expressed in a patient sample.
Mray PCR probes are useful for diagnosing diseases, and can characterise
the response of the infectious organism to drugs. Mray proteins and
polymucleotides are also useful for screening for antagonists, agonists
and drugs against infectious micro-organisms. Mray agonists and
antagonists are bacteriostatic and bacteriocidal compounds which can be
sequence) mray activity, therefore treating microbial diseases,
sequence) mray activity, therefore treating microbial diseases,
especially Streptococcus pneumoniae diseases including otitis media,
bacteraemia, conjunctivitis, pneumonia, sinusitis, pleural empyema,
condocarditis and especially meningitis. Epitopes of mray proteins and
polynucleotides are useful immunogens (vaccines) for producing anti-mray
polynucleotides can be used in genetic immunisation (gene therapy) to
prevent infections. Mray proteins, polynucleotides and their
control provent infections. Mray proteins, and
control advession of bacterial to matrix proteins, and
control are assetul for use on wounds and body implants to prevent bacterial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Thanassi JA;
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48.0%; Score 47; DB 20; Length 326;
Best Local Similarity 43.8%; Pred. No. 17;
Matches 7; Conservative 5; Mismatches 4; Indels
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141 YQVHLGIFYIVFALFW 156
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Appression, where too status for the presence of proteins essential for the viability of a bacterial cell wall in samples such as cells, tissues, biological fluids, blood, serum, nose, ear or throat swabs with ligands, and for detecting corresponding target nucleic acid molecules with complementary sequences. The nucleic acids are also useful for determining whether a genomic nucleotide sequence of interest is essential for viability of a bacterial cell or whether it resides within an operon, by integrating an exogeneous nucleotide sequence comprising a portion of an open reading frame of the genomic sequence of interest comprising 200-500 base pairs) into the genomic sequence of interest which confers a selectable phenotype to the cell, and determining cell viability with a selection agent such as chloramphenicol. The nucleic acids and proteins are also useful as vaccines and for treating bacterial infections with gene therapy and antisense therapy. The nucleic acids antibiotic resistant bacterial infections.
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Expression", where CEG stands for "Conserved Essential Gene". The nucleic
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                                                                                                                                                                                                                                                                                                            48.0%; Score 47; DB 22; Length 326;
43.8%; Pred. No. 17;
1ive 5; Mismatches 4; Indels
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2000US-0198123.
2000US-0205515.
2000US-0209467.
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2000US-0215135.
2000US-021647.
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2000US-0189874
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Matches 7; Conserv
                                                                                                                                                                                                                                                                                 326 AA;
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18-APR-2000;
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AAM84080
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2000US-0229345.
2000US-0229509.
2000US-0229513.
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2000US-0234274.
2000US-0234997.
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2000US-0236367.
2000US-0236368.
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2000US-0232081
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2000US-0233063
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2000US-0235836
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2000US-0237039
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2000US-0239935
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2000US-0246525
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             14-AUG-2000;
14-AUG-2000;
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22-AUG-2000;
22-AUG-2000;
22-AUG-2000;
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33-AUG-2000;
11-SEP-2000;
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25-SEP-2000;
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27-SEP-2000;
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29-SEP-2000;
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08-NOV-2000;
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2000US-0249212.
2000US-0249213.
2000US-0249214.
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2000US-0249209.
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2000US-0249264.
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08-NOV-2000;
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01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
                                                                                                 17-NOV-2000;
17-NOV-2000;
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                                                                                              .7-NOV-2000;
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Claim 11; SEQ ID NO 11673; 3071pp + Sequence Listing; English.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Rosen CA, Barash SC, Ruben (HUMA-) HUMAN GENOME SCI INC.

WPI; 2001-483426/52. N-PSDB; AAK56861.

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) colynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to produce the call to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially concern acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-derived cells. AAK64703 concerns and canner metastases of haematopoietic derived cells. AAK64703 concerns cell to proceed to the present invention. AAK84942 to AAK87650 and AAM82169 represent sequences used in the exemplification of the present invention.

Sequence

AAB57264

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Anti-CD4 antibody; monkey; human; therapy; variable heavy domain; old World monkey; constant domain; eczema; immuno-modulated disease;
                                                                                                                                                                                                                   Anti-CD4 antibody VH5 monkey clone 5-11.
                                                                                                             AAW54009 standard; Protein; 123 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 9e; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Raab RW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    910S-0735064.
920S-0856281.
950S-0379072.
950S-0476349.
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                                                                                                                                                                                   (first entry)
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ESNCGLDFVSFF 40
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                                                                                                                                                                                                                                                                                         rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Newman RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-296690/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JUL-1991;
23-MAR-1992;
05-DEC-1995;
07-JUN-1995;
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                                                                                                                                                AAW54009;
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                                                                                              AAW54009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF15566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gyaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other disgnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, reproductive, disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                         neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease.
                                                                                                                                                                                                                                                                                                                                                            Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of
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                                                                                                                                                                                                                                                                                                                         Human prostate cancer antigen protein sequence SEQ ID NO:1842.
                      22; Length 50;
                                                         Indels
                                                         3,
                      Score 46; DB
Pred. No. 4.1;
                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 2304; 2338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer antigens, useful for treatmen
disorders such as prostate cancer
                                                                                                                                                                                                                 AAB57264 standard; Protein; 64 AA.
                    46.98;
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                                                                                                                                                                                                                                                                                     (first entry)
Ouery Match
Best Local Similarity 46.2-
Best Conservative
The Conservative
                                                                                        4 NCGIDFIIFWIFW 16
                                                                                                                          12 NCCYOFLIFFLYW 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-587513/55.
N-PSDB; AAF16467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200055174-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                     13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-SEP-2000.
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                                                                                                                                               This sequence represents the VH5 domain of an anti-CD4 antibody (Ab). This sequence can be used in the method of the invention for treating a subject, where the treatment comprises administration of an antibody which has an Old World monkey (e.g. baboon or macaque) variable region which binds to an antigen (Ag) (or Ag binding portion), and a human constant domain. The method is useful for the treatment of eczema and immuno-modulated diseases and especially rheumatoid arthritis. The recombinant antibodies used are sufficiently different from native monkey antibodies to allow human antigens to raise these antibodies, but similar enough to human antibodies used in therapy in prior art, these antibodies do not antibodies used in therapy in prior art, these antibodies do have longer half-lives and do not have a lack of effector function with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Improved method for antibody treatment – uses an antibody comprising an Old World monkey variable region and a human constant domain
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ID AAM51648 standard; Protein; 285 AA.
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Matches 7; Conservative
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Conservative

Best Local Similarity Matches 6; Conserv

64 AA;

Sequence Query Match ö

Gaps

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1; Indels

46.9%; Score 46; DB 21; Length 64; 50.0%; Pred. No. 5.1;

Mismatches

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10-SEP-1992;
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WO9405695-A1
                                                                                          10-SEP-1992;
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                             17-MAR-1994.
                                                                                                                                                       Murphy RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW02727;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated human G protein-coupled receptor subfamily. The polypeptide comprises a fully defined sequence of 289 amino acids as given in the specification, or its fragment comprising 10 contiguous amino acids, or an amino acid sequence of an allelic variant or orthologue of the amino acid sequence given in the sequence. The polypeptide is useful for identifying a modulator of a GPCR polypeptide or an an agent that binds too it. The polypeptide is also useful for treating a disease or condition mediated by human proteases. The present sequence is a rat GPCR polypeptide used in comparison studies with the polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G-protein coupled receptor; ligand binding assay; transmembrane domain; psychotic disorder; schizophrenia; dopamine; cAMP; adenosine; thrombin; muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine; rhodopsin; opsin; odorant; cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human G protein-coupled receptor polypeptide that is related to MAS proto-oncogene receptor subfamily, useful as model and target for developing human therapeutic agent -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.9%; Score 45; DB 23; Length 285; 60.0%; Pred. No. 30; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human thoracic aorta G-protein coupled receptor protein.
                                                                                                                           MAS proto-oncogene receptor; human protease; disease.
                                                                                                            Rat; G-protein coupled receptor; GPCR; gene therapy;
                                                                                                                                                                                                                                                                                                                                                             Di Francesco V, Beasley EM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR48755 standard; Protein; 298 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 2; 60pp; English.
                                                                                                                                                                                                                                                   24-APR-2001; 2001WO-US13097.
                                                                                                                                                                                                                                                                                24-APR-2000; 2000US-199149P.04-AUG-2000; 2000US-0633146.
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                                               (first entry)
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213 GIDWFLFWVF 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 GIDFIIFWIF 15
                                                                               Rat GPCR polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                             Cravchik A,
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-049265/06.
                                                                                                                                                                                                                                                                                                                               (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          285 AA;
                                                                                                                                                                                       WO200181409-A2.
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                                               20-FEB-2002
                                                                                                                                                                                                                      01-NOV-2001.
                                                                                                                                                           Rattus sp.
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                 AAM51648
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proteins selected from CAMP, adenosine, muscarinic acetylcholine, adrenergic thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin, addrant, cytomegaloviral and other G-protein coupled receptors. The receptor proteins were used to design polypeptides, pref. based on the transmembrane domains, for use in G-protein coupled receptor ligand blinding assays. The polypeptide fragments retain biological activity such as binding agent ligand or modulating GPR ligand binding to a GPR (see AAR48759-R48758, AAR50569-R50807 and AAR89189-R89195 for examples of polypeptide fragments can be used in compositions for treating subjects suffering from a pathology related to a GPR abnormality e.g. a psychotic disorder such as schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proteins AAR48685-R48758 represent a range of G-protein coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G-protein coupled receptor; ligand binding assay; transmembrane domain; schizophrenia; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin; muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin; odorant; cytomegalovirus; serotonergic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                   Polypeptides of G-coupled receptor proteins (GPRs) - useful for
binding GPR ligands or modulating GPR binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human thoracic aorta G-protein coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 130-131; 160pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 45.9%;
Best Local Similarity 60.0%;
Matches 6; Conservative
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                                                                                                                                               (UYNY ) UNIV NEW YORK STATE.
93WO-US08528
                                                                         92US-0943236.
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                                                                                                                                                                                                                      Schuster DI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||: :||:|
211 GIDWFLFWVF 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 GIDFIIFWIF 15
                                                                                                                                                                                                                                                                                    WPI; 1994-101120/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 AA;
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                                                                                                                    Proteins AAW02657-W02730 represent a range of G-protein coupled receptor defensely. Aromain, endothelin, bombesin, endocrine, rhodopsin, opsin, odorant, cytomegaloviral and other GPR proteins. The receptor proteins were used to design polypeptides, pref. based on the transmembrane domains, for use in G-protein coupled receptor ligand binding assays. The polypeptide fragments retain biological activity such as binding a GPR 14gand or modulating GPR 11gand binding to a GPR (see AAW02247-W0299) for examples of polypeptide fragments). The polypeptide fragments can be used in compositions for treating subjects suffering such as schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                signal processing; female reproductive tissue; infertility; cardiovascular disease; coronary heart disease; heart attack; stroke; inflammatory disorder; metabolic disorder; utenus; placenta; ovary; prostate; reproductive disorder; pain; cancer; CNS disorder; ovary; prostate; reproductive disorder; pain; cancer; CNS disorder; contral nervous system disorder; schizophrenia; episodic paroxysmal anxiety; EPA, obsessive compulsive disorder; CDD; Parkinson's disease; multiple sclerosis; Alzheimer's disease; dementia; Huntingdon's disease; anorexia; kidney disease; renal failure; obesity; astrointestinal disorder; irritable bowel syndrome; IBS; diarrhoea; allergy; arthritis; sepsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G-protein coupled, receptor; IGPcR18; cardiovascular system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                 New dopamine receptor peptide - useful as antipsychotic agent, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human G protein-coupled receptor protein, IGPCR18, useful for diagnosis, prevention, amelioration or treatment of pain, cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                              45.9%; Score 45; DB 17; Length 298; 60.0%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human G-protein coupled receptor IGPCR18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wattler F, Wattler S, Trommler P, Nehls MC;
                                                                                  Disclosure; Column 173-176; 184pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU76411 standard; Protein; 323 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUL-2001; 2001WO-EP07530.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-2000; 2000US-215879P.
                                                      for treating schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 GIDWFLFWVF 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 GIDFIIFWIF 15
WPI; 1996-208785/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-140079/18
                                                                                                                                                                                                                                                                                                                                                          298 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU76411;
                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
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in female reproductive tissues, such as infertility, cardiovascular diseases such as coronary heart disease, heart attack and stroke, conflammentry disorders and metabolic disorders linked to reproductive tissues like uterus, placenta, ovary and prostate, reproductive disorders, pain, cancer, central nervous system disorders such as schizophrenia, episodic paroxysmal anxiety (EPA) disorders such as schizophrenia, episodic paroxysmal anxiety (EPA) disorders such as schizophrenia, episodic paroxysmal anxiety (EPA) disorders such as schizophrenia, alsease, dementia, Huntington's disease, anorexia, kidney diseases such as renal failure, obesity, gastrointestinal cdisorders such as renal failure, observity, gastrointestinal cdisorders such as renal failure, observity, gastrointestinal cdisorders and conditions of delayed gastric emptying, osteoporosis, infections such as paramed in for the disorders and conditions of delayed gastric emptying, osteoporosis, asthma, allergy, arthritis, and sepsis. (I) is useful for the production of other cellular gene products involved in regulating IGPORIB, and as pharmaceutical reagents. (II) is useful for mapping the location of the gene to the chromosome, and to detect abnormalities involving IGPORIB gene structure. This continual is the anino acid sequence of the novel human of protein coupled receptor, and the anino acid sequence of the novel human of protein coupled receptor, and an acid sequence of the novel human of protein coupled receptor, and an acid sequence of the novel human of ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                colon; small intestine; stomach; mammary gland; prostate; testis; psychiatric disorder; central nervous system disorder; schizophrenia; episodic and paroxysmal anxiety disorder; Parkinson's disease; multiple sclerosis; Alzheimer's disease; cardiovascular disease; nearline; angina pectoris; kidney disease; dyslipidaemias; obesity; emesis; gastrointestinal disorder; inflammatory bowel disease; diabetes; osteoporosis; inflammation; infection; human immunodeficiency virus; HIV; cancer; immune disorder; urinary retention; asthma; allergy; arthritis; benign prostatic hypertrophy; endotoxin shock; sepsis; gene therapy; gynaecological disorder; vaccine; human.
                                                                                                                                      The invention describes a novel human G protein-coupled receptor (GPCR) protein, IGPCR18 (1). (1), the polynucleotide (II), agonists and antagonists of (I)/(II) are useful for the diagnosis and treatment of cardiovascular system disorders, the detection of mutant or inappropriately expressed forms of IGPCR18, and for drug screening. (I) is useful in treatment of diseases associated with signal processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45; DB 23; Length 323;
Pred. No. 34;
3; Mismatches 1; Indels
inflammatory, metabolic, reproductive, gynaecological, and cardiovascular disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPcR18, described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human G-protein coupled receptor, IGS43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE14729 standard; Protein; 327 AA.
                                                                                  Claim 8; Fig 2; 55pp; English.
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60.0%;
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Best Local Similarity 60...
6; Conservative
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238 GIDWFLFWVF 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200228897-A2.
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AAE14729
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02-OCT-2000; 2000EP-0203411.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to IGS43 G-protein coupled receptor (GPCR) and the polynucleotide encoding it. The IGS43 polypeptide, polynucleotide, agonist, antegonist or antibody is useful for treating dysfunctions or agonist, antegonist or antibody is useful for treating dysfunctions or intestine, stomach, mammary gland, prostate, testis, central nervous system, cerebellum and spinal cord. The polypeptide is useful as vaccine for inducing immunological response in a mammal, for treating psychiatric and central nervous system disorders including schizophrenia, episodic and paroxysmal anxiety disorders e.g. obsessive compulsive disorder, bipolar disorder, parkinson's disease, general anxiety disorder, bipolar disorder, parkinson's disease, general cancier, bipolar disorder, parkinson's disease, dementia, severe mental retardation, Huntington's disease, disease, danentia, severe mental retardation, autington's disease, disease, antiem, edition, dependency/craving, sleep disorder, epilepsy, migraine, attention deficit/hyperactivity disorder, cardiovascular diseases including heart failure, angina pectoris, subarchnoid haemornhage, cerebral ischaemia, cerebral infarction, phyertension, thrombosis, arterioscalerosis, cerebral infarction, errobral infarction, disease, kidney disease, dysliphdaemias, obesity, emesis, gastrointestinal disease, diabetic correction, critical propers, including disease, diabetic including critical propers, including critical disease, diabetic including critical propers, and disease, diabetic including critical disease, diabetic disease, and disease, diabetic including critical disease, diabetic disease, and disease, diabetic disease, and disease diabetic disease.
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                                                                                                                                                                                                                                                                                          Novel G-protein coupled receptor, termed IGS43 polypeptide and nucleic acid encoding the polypeptide, useful for treating disorders of uterus, kidney, lung, colon, stomach, mammary gland, prostate and testis -
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                                                                                                                                    De Moor L;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 25; Page 7; 59pp; English.
   04-OCT-2000; 2000US-237394P.
                                                                                                                                 Deleersnijder W, Blockx H,
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Matches 6; Conservative
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                                                                     (SOLV ) SOLVAY PHARM BV.
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N-PSDB; AAD31159.
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G protein coupled receptor (GCR) proteins can be used to identify ligands which act as antagonists of GCR/ligand binding. Such ligands can be used for promoting or inhibiting physiological responses such as liberation of arachidonic acid, acetylcholine and endocellular calcium, endocellular cyclic AMP production, production of inositol, changes in cell membrane potential, phosphorylation of endocellular protein and cell promulgation. The GCR products can also be used for the detection of ligands and in the production of antibodies and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
G protein coupled receptor protein; GCR; identification; detection; ligands; physiological response; arachidonic acid; acetylcholine; calcium; cyclic adenosine monophosphate; cAMP; inositol; membrane potential; phosphorylation; c-fos; antibodies;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated rabbit G protein receptor protein – used partic. to identify agonists or antagonists which can promote or inhibit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fuji R, Hinuma S, Kawamata Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                             95EP-0117786.
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Matches 6; Conservative
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256 GIDWFLFWVF 265
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                                                                                                                                                                                                  Oryctolagus cuniculus
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Job time: 9.92035 secs
                                                                                                                                            transgenic animals.
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Sequence 15, Sequence 13, Sequence 21, Sequence 21, Sequence 4, A Sequence 4, A Sequence 15, Sequence 15, Sequence 2, A Sequence 2, A Sequence 24, Sequence 5, A Sequence

Sequence

ALIGNMENTS

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94.994 Million cell updates/sec
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
          5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-478-039-82
US-08-176-349A-82
US-08-118-270-76
US-08-118-270-76
US-08-655-202-46
US-08-665-202-46
US-08-665-202-46
US-08-665-202-46
US-08-665-202-46
US-08-118-157B-12
US-08-118-157B-12
US-08-118-157B-12
US-08-118-157B-12
US-08-65-202-52
US-08-65-202-53
US-08-65-202-53
US-08-65-202-54
US-08-65-202-55
US-08-65-202-57
US-08-118-157B-9
US-08-318-157B-9
US-08-318-157B-11
                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                      262574 segs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
          GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                          protein search, using sw model
                                                                                 9, 2003, 15:05:28
                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                 US-09-854-133-587
98
1 FQANCGIDFIIFWIFW 16
                                                                                                                                                                                                                                                                                                                                                            Issued_Patents_AA:*
                                                                                                                                                                                                                                                                      Minimum DB seq length: 0 Maximum DB seq length: 20000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match Length
                                                                                    July
                                                                                                                                                                                  Scoring table:
                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                           ı
                                                           OM protein
                                                                                                                                                           Sequence:
                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                            Database
                                                                                    ou:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Result
No.
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Sequence 82, Appl Sequence 76, Appl Sequence 76, Appl Sequence 45, Appl Sequence 49, Appl Sequence 51, Appl Sequence 51, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 52, Appl Sequence 52, Appl Sequence 53, Appl Sequence 54, Appl Sequence 57, Appl Sequence 57, Appl Sequence 57, Appl Sequence 67, Appl Sequence 67, Appl Sequence 67, Appl Sequence 67, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl

US-08-476-349A-82

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                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: Newman, Roland A.

APPLICANT: Newman, Nabil

APPLICANT: Raab, Nabil

APPLICANT: Raab, Nabil

APPLICANT: Rab, Nabil

APPLICANT: Hanna, Nabil

APPLICANT: Hanna, Nabil

APPLICANT: Hanna, Nabil

APPLICANT: Hanna, Nabil

APPLICANT: Rab, Nabil

CORRESPONDENCES: 114

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince St.

CITY, Alexandria
                                                                                                                                                                        Length 123;
                                                                                                                                                                                                                  5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STAIL:
COUNTRY:
11: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORFATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION NOWER: US/08/476,349A
FILING DATE: 07-JUN-1995
FILING DATE: 07-JUN-1995
                                                                                                                                                                      Score 46; DB 1;
Pred. No. 3.9;
                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35,030
35,030
4FR: 012712-161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATYORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161
TELECOMMUNICATION INFORMATION:
                                                        ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: VH5 clone 5-11
US-08-478-039-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHROMOSOME/SEGMENT: VH5 clone 5-11
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 82, Application US/08476349A Patent No. 5750105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: not relevant TOPOLOGY: not relevant
                                                                                                                                                                    Query Match 46.9%;
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 123 amino acids
amino acid
not relevant
3: peptide
                                                                                                                                                                                                                                                       5 CGIDFIIFWIFW 16
                                                                                                                                                                                                                                                                                               25 CGFSFTGFWISW 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Monkey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POSITION IN GENOME
                   MOLECULE TYPE: E
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                                                                                                                                                                                                                                                                                                                                                            RESULT 2
US-08-476-349A-82
TOPOLOGY:
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Sequence 76, Application US/08118270

Sequence 76, Application US/08118270

Patent No. 5508384

GENERAL INFORMATION:

APPLICANT: Murphy, Randall B.

APPLICANT: Schušter, David I.

TITLE OF INVERTION: POLYEPETIDES OF G-COUPLED PROTEIN

TITLE OF INVERTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF

NUMBER OF SEGUENCES:

ADDRESSEE: BROWDY AND NEIMARK
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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0
Length 123;
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                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER REALIBLE FORM
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-TOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: TOWNSENG, KEVIN G.
REGISTRAION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MRRPHY=2A
TELEFRONE: 202-628-5197
TELEFRONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                             ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
 Score 46; DB 1;
Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45; DB 1;
Pred. No. 14;
                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
46.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                    Conservative
                                                                                         25 CGFSFTGFWISW 36
                                                                 5 CGIDFIIFWIFW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: peptide US-08-118-270-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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211 GIDWFLFWVF 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 GIDFIIFWIF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
6; Conserve
Query Match
Best Local Similarity
Matches 7; Conserv
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STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                    D.C.
                                                                                                                                                                                                                                                                                                                                                                                                              20004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                      RESULT 3
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-665-202-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.9%; Score 45; DB 5; Length 298; 60.0%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                              MEDIUM TYPE: Floppy disk Compatible Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATPONNEY/AGENT INPOMMATION:
NAME: TOWNSHOM KEVIN G.
REGISTRATION NUMBER: 34,033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT TELEPONMUNICATION INFORMATION: TELEFAX: 202-628-5197
TELEEX: 248633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UMBER: US 60/000,238
14-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-665-202-45
; Sequence 45, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
                   BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 248633
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: peptide PCT-US93-08528-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
CORRESPONDENCE ADDRESS:
                                                                                                                               COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 GIDFIIFWIF 15
                                                     Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                             20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGIH:
                                 STREET:
                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Sequence 46, Application US/08665202
Fatent No. 597322
GENERAL INFORMATION
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: Tumor No. 5977322el High Affinity Human Antibodies to TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB 2; Length 125;
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1:0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202 FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 45:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 46:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                   42.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                i: 125 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 125 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 54...
                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-665-202-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 GIDFIIFWIFW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 GYDFTTYWIAW 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        San Francisco
California
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APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Seed, Brian
APPLICANT: Holgersson, Jan
APPLICANT: HOLGERSON, Jan
TITLE OF INVENTION: FUCOSYLTRANSFERASE GENES AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42; DB 2; Length 125;
Pred. No. 16;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.30
                                                                                                                                              Townsend and Townsend and Crew LLP
                                                                                                                                                               STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FAZERLIN RELEASE #1.0, VET CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202 FILING DATE: 13-UN-1996 CLASSIFICATION 424 PRIOR APPLICATION NUMBER: US 60/000,238 FILING DATE: 14-UN-1995 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250 FILING DATE: 15-UN-1995 FILING DATE: 15-UN-1995 ATTORNEY,AGENT INFORMATION:
                                                                                                                                                                                                                                              ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 2, Application US/08483151
; Patent No. 5858752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 0.
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 125 amino acids
amino acid
                                                                                                    NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: peptide US-08-665-202-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 GIDFIIFWIFW 16
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  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                   usa
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                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                       Sequence 49, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to TIVENE OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
                                                                                                        Gaps
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                                                          Score 42; DB 2; Length 125;
Pred. No. 16;
1; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/665,202

FILING DATE: 13-JUN 1996

CLASSIFICATION: 424

PRIOR APPLICATION UMBER: US 60/000,238

FILING DATE: 14-JUN-1995

PRIOR APPLICATION NUMBER: US 60/000,250

APPLICATION NUMBER: US 60/000,250

FILING DATE: 15-JUN 1995

ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 16;
l; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 51, Application US/08665202 Patent No. 5977322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
                                                             42.9%;
54.5%;
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54.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 4 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 amino acids
                                       Ouery Match
Best Local Similarity 54.5.
Accorded by Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 54.5
Matches 6; Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                6 GIDFIIFWIFW 16
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26 GYDFTTYWIAW 36
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26 GYDFTTYWIAW 36
; MOLECULE TYPE: peptide US-08-665-202-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                      US-08-665-202-49
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Gaps

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ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/464
                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                             28,665
                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION TELEPHONE: (202)672-5300 TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Foley & Lardner
                                                                                                                    STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,6
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.98;
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ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             I: 119 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 42.9
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                     NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-318-1578-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                     Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 05 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-318-157B-12
                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                STREET:
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Sequence 4069, Application US/09134001C

Sequence 4069, Application US/09134001C

Sequence 4069, Application US/09134001C

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (6) ... A OTHER INFORMATION: Identity of amino acid at the above locations are unknown. US-09-134-001C-4069
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Patent No. 5874540
GENERAL INFORMATION:
APPLICANT: HANSEN, Hans J.
APPLICANT: ARMONER, Kathryn L.
TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
                                                                                                                                                                                                                                                                                                                                                                                                                             42.9%; Score 42; DB 2; Length 342; 45.5%; Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.9%; Score 42; DB 4; Length 518; 58.3%; Pred. No. 69; 3; Indels tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                          REFERENCE/DOCKET NUMBER: 00786/278001
ELECOMMUTCATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPRAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
LENGTH: 518
                               UMBER: US/08/483,151
07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Staphylococcus epidermidis
                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER: 35,238
                                                                                                                                                                                                                       TELEFAX: 617/542-8906
TELEEX: 200154
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                         : 342 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 58...
7; Conservative
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              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 07-JUN-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | | |:: | ||
21 GATFMVIWFFW 31
                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                    linear
                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                           CENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Patent No. 5874540
GENERAL INFORMATION:
APPLICANT: HANSEN, Hans J.
APPLICANT: ARMOUR, Kathryn L.
TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
TITLE OF INVENTION: MOUSE MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Indels
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                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: US/08/318,157B FILING DATE: U5-02-1994 CLASSIFICATION: 424
TITLE OF INVENTION: MOUSE MONOCLONAL ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB Pred. No. 21; 2; Mismatches
                                                                       E: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3000 K Street, N.W., Suite 500
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STRANDEDNESS:
                          JS-08-665-202-48
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APPLICANT: HANSEN, Hans J.

APPLICANT: HANSEN, HALS J.

APPLICANT: ARMOUR, KALHYDL L.

TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESSE: FOLEY & Lardner

STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                    Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41; DB 2; Length 119; Pred. No. 21;
                                                                                                                                                                                                                                                                      5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA

ZIP: 20007-5109

COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,157B
FILING DATE: 0-C-CT-1994
ATONNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard 0.
REGISTRATION NUMBER: 28,665
REGISTRATION NUMBER: 28,665
REBERNOE/DOCKET NUMBER: 18733/464
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: (202)672-5399
                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                                                  Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17, Application US/08318157B Patent No. 5874540
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5390
TELETAX: 904136
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 annino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 904136
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
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23 SSGFDFTTYWMSW 36
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23 SSSGFDFTTYWMSW 36
                                                                                                                                                                                                              Query Match
Best Local Similarity 35./-
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Best Local Similarity 35.7
Matches 5; Conservative
                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-318-1578-17
                                                                                                                                                                linear
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                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                              US-08-318-157B-12
                                                                                                                                                              TOPOLOGY:
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STATE: D.
COUNTRY:
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Sequence 48, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 50, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41; DB 2; Length 125; Pred. No. 22;
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/665,202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco CITY: California COUNTRY: USA
                                                                                                                                                                                ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02307E-061410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-UNN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-UNN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 48:
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54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 41.8
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: peptide US-08-665-202-48
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94111-3834
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COMPUTER READBLE FORM:

MEDIOUR TYPE: FORPY

MEDIOUR MEDION DATA:

APPLICATION NUMBER: US 60/000,238

FILING DATE: 13-JUN-1995

PRIOR APPLICATION NUMBER: US 60/000,238

FILING DATE: 11-JUN-1995

PRIOR APPLICATION NUMBER: 02 60/000,250

PRIOR APPLICATION NUMBER: 03 60/000,250

PRIOR APPLICATION NUMBER: 03 60/000,250

ATOMNEC/AGENT INFORMATION: 84,488

MEDIOR MEDIOR INFORMATION: 18,500

MARE: MAINTENANCE/AGENT INFORMATION: 19,500

MARE: MAINTENANCE/AGENT INFORMATION: 10,500

MAINTENANCE/AGENT INFORMATION: 11,500

MAINTENANCE/AGENT
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 9, 2003, 15:06:38; Search time 5.38053 Seconds Run on:

(without alignments)
346.196 Million cell updates/sec

US-09-854-133-587 98 Title: Perfect score:

1 FQANCGIDFILFWIFW 16

Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

445758 seqs, 116419773 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Database :

Published_Applications_AA:*

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2: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	Sequence 587, App	Sequence 587, App	Sequence 587, App	Sequence 586, App	Sequence 586, App		Sequence 742, App	Sequence 1842, Ap	Sequence 90, Appl	Sequence 4, Appli	Sequence 4, Appli	Sequence 2, Appli	0,	2,	6	482	Sequence 2, Appli	6	Sequence 2, Appli
	ID	US-09-854-133-587	US-10-144-649A-587				US-09-738-973-586	_		US-09-850-165-90	_		US-10-176-079-2	US-10-176-079-9	US-09-929-752-2	US-09-929-752-9	US-10-225-567A-482	US-10-184-426-2	US-10-184-426-9	US-09-985-694A-2
	DB	6	σ	10	σ	σ	10	σ	10	10	Φ			Q	σ	0	Φ	6	σ	10
	Query Match Length DB	16	16	16	97	97	97	114	64	123	323	323	343	343	343	343	343	343	343	343
æ	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	46.9	46.9	45.9	45.9	45.9	45.9	45.9	45.9	45.9	45.9	45.9	45.9
	Score	86	86	86	86	86	86	86	46	46	45	45	45	45	45	45	45	45	45	45
	Result No.	1	7	3	4	2	9	7	8	6	10	11	12	13	14	15	16	17	18	19

Sequence 973, Apple Sequence 973, Apple Sequence 11503, A Sequence 118, Apple Sequence 118, Apple Sequence 132, Apple Sequence 1073, Apple Sequence 17, Apple Sequence 17, Apple Sequence 17, Apple Sequence 17, Apple Sequence 51, Apple Sequence 61, Apple Sequence 81, Apple 81,	Sequence 11, Appl Sequence 13, Appl Sequence 14, Appl
US-09-985-694A-9 US-09-925-299-973 US-09-925-299-973 US-09-815-242-11503 US-09-815-242-11503 US-09-815-242-11388 US-09-815-242-11388 US-09-789-561-132 US-09-789-561-132 US-09-789-561-132 US-09-789-694-4 US-10-191-504-1073 US-09-253-794-2 US-09-253-794-12 US-09-253-794-12 US-09-253-794-12 US-09-804-291-485 US-09-804-291-485 US-09-804-291-485 US-09-804-291-485 US-09-804-291-485 US-09-253-794-10	mmm
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Gaps
                                                                                   APPLICANT: Loddes, Michael J.
APPLICANT: Mohamath, Raodoh
APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Pobert A.
APPLICANT: Benson, Darin R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSTS OF LUNG CANCER
TITLE OF INVENTION: UMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SEQ ID NO S87
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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100.0%; Pred. No. 1.5e-08;
tive 0; Mismatches 0;
                   ; Sequence 587, Application US/09854133; Publication No. US20020183499A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          CRGANISM: Homo sapiens
US-09-854-133-587
US-09-854-133-587
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Sequence 587, Application US/10144649A; Publication No. US20030118599A1; GENERAL INFORMATION: APPLICANT: Lodes, Michael J.
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Algate, Paul A.
APPLICANT: McNeill, Patricia D. 1 FQANCGIDFIIFWIFW 16 1 FOANCGIDFILFWIFW 16 US-10-144-649A-587 δ qq

us-09-854-133-587.rapb

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Fatent No. US20020110563A1

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Applicant, Randoh
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Andiate, Paul A.
APPLICANT: Andiate, Paul A.
APPLICANT: Mohamath, Randoh
APPLICANT: Andiate, Paul A.
APPLICANT: Mohamath, Randoh
APPLICANT: Algate, Paul A.
APPLICANT: Mohamath, Mark
APPLICANT: Manion, Jane
APPLICANT: Manion, Jane
APPLICANT: Manion, Jane
APPLICANT: Algate, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CURRENT FILING DATE: 2000-12-14
CURRENT APPLICATION NUMBER: US/09/738,973

NUMBER OF SEQ ID NOS: 587

NUMBER OF SEG ID NOS: 587
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER FILE REPERENCE: 210121.1475C11
CURRENT APPLICATION NUMBER: US/10/144,649A
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 749
SOFTWARE: FRSTSEQ for Windows Version 3.0
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Darin R.
APPLICANT: Secrist, Heath R.
APPLICANT: GEORIST: HEATHORS FOR TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 16;
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                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                       100.0%; Score 98; DB 9; I 100.0%; Pred. No. 1.5e-08;
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Pred. No. 1.5e-08;
                                                                                                                                                                                                                                                                                                                                                       Mismatches
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; Publication No. US20020183499A1
; GENERAL INFORMATION:
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100.0%;
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                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                          TYPE: PRT
CORGANISM: Homo sapiens
US-10-144-649A-587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-738-973-587
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LENGTH: 16
                                                                                                                                                                                                                                                                                                         Query Match
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 586, Application US/10144649A
; Sequence 586, Application US/10144649A
; Publication No. US20030118599A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
APPLICANT: Wang, Tongtong
; APPLICANT: Pan, Liqun A.
; APPLICANT: Algare, Paul A.
; APPLICANT: Algare, Paul A.
; APPLICANT: Algare, Paul A.
; TILLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; TILLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF CURRENT APPLICATION NUMBER: US/10/144,649A
; CURRENT APPLICATION NUMBER: US/10/144,649A
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 749
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 586
LENGTH: 97
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APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C9
                                                                                                                                                                                                                                          Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 97;
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                                                                                                                                                                                                                                   Query Match 100.0%; Score 98; DB 9; 1 Best Local Similarity 100.0%; Pred. No. 7.8e-08; Matches 16; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 7.8e-08;
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                  CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 586
LENGTH: 97
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/09/738,973
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; Patent No. US20020110563A1
; GENERAL INFORMATION:
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Secrist, Heather
Indirias, Carol Yoseph
Benson, Darin R.
Elliot, Mark
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Henderson, Robert A.
Lodes, Michael J.
Fling, Steven P.
Mohamath, Raodoh
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FILE REFERENCE: 210121.475C10
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                         ; ORGANISM: Homo sapiens US-09-854-133-586
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Algate, Paul A.
APPLICANT: MONEIL, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475111
CURRENT APPLICATION NUMBER: US/10/144,649A
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 749
SOFTWARE: FastSEQ for Windows Version 3.0
SERVICE OF SEQ ID NOS: 749
SERVICE OF SEQ ID NOS: 749
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APPLICANT: Steve Ruben
TILE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1909-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Petentin Ver. 2.0
SEQ ID NO 1842
LENGTH: 64
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CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 587
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 586
LENGTH: 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 742, Application US/10144649A Publication No. US20030118599A1 GENERAL INFORMATION:
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Best Local Similarity 100.0%; P
Matches 16; Conservative 0;
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Best Local Similarity 100.0
Matches 16; Conservative
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US-10-144-649A-742
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US-09-925-300-1842
                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-738-973-586
                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
US-10-144-649A-742
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                                                                                                                       TYPE: PRT
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Fublication No. US20030059891A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WEL, Ming-Hui
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
GURRENT APPLICATION NUMBER: US/10/266,643
CURRENT APPLICATION NUMBER: US/10/266,643
CURRENT FILING DATE: 2002-10-09
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
SEQ ID NO 4
SEQ ID NO 4
SEQ ID NO 4
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                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: NEWMAN, ROLAND A.
APPLICANT: HANNA, NABIL
APPLICANT: RAAB, RONALD W.
TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
ELLE REFERENCE: 037003-0280614
CURRENT APPLICATION NUMBER: US/09/850,165
CURRENT FILING DATE: 2001-05-08
  DB 10; Length 64;
                                                      1; Indels
Score 46; DB Pred. No. 4; 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2001-05-08
PRIOR APPLICATION NUMBER: 09/082,472
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 08,476,237
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08,730,772
PRIOR FILING DATE: 1995-04-17
PRIOR FILING DATE: 1995-04-17
PRIOR FILING DATE: 1995-07-10
PRIOR FILING DATE: 1992-07-10
PRIOR FILING DATE: 1992-07-13
PRIOR FILING DATE: 1992-07-13
PRIOR FILING DATE: 1992-07-16
PRIOR FILING DATE: 1992-07-16
PRIOR FILING DATE: 1991-07-25
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTIN NUMBER: 07/735,064
                                                                                                                                                                                                                                                                                                Sequence 90, Application US/09850165 Patent No. US20020150580A1
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  46.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 58.3
Matches 7; Conservative
  Query Match
Best Local Similarity 50.0
Matches 6; Conservative
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US-09-850-165-90
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TYPE: PRT
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Sequence 4. Application US/09816087

Patent No. US20020064822A1

GENERAL INCOMPTION:
GENERAL INCOMPTION:
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED

TITLE OF INVENTION: PROTEINS, AND USES THEREOF

FILE REPERENCE: CLO00749-CIP

CURRENT FILING DATE: 2001-03-26

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastseQ for Windows Version 4.0

SEQ ID NO 4
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Pred. No. 25;
Query Match 45.9%; Score 45; DB 9; Length 323; Best Local Similarity 60.0%; Pred. No. 25; Matches 6; Conservative 3; Mismatches 1; Indels
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Pred. No. 27;
3; Mismatches 1; Indels
                                       1; Indels
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60.0%;
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; ORGANISM: Rattus norvegicus
US-09-816-087-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 60.07
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Best Local Similarity 60.0
Matches 6; Conservative
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244 GIDWFLFWVF 253
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244 GIDWFLFWVF 253
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256 GIDWFLFWVF 265
                                                                    6 GIDFIIFWIF 15
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                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 323
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US-10-176-079-9
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Gaps
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09929752
Publication No. US20030113909A1
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
Kawamata, Yuji
TITLE OF INVENTION:
PRODUCTION AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.9%; Score 45; DB 9; Length 343; 60.0%; Pred. No. 27;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                            GENERAL AINCURSTANCE.

APPLICANT: Li et al.

TITLE OF INVENTION: G-Protein Coupled Receptor
FILE REFERENCE: PP145P1012.

CURRENT APPLICATION NUMBER: US/10/176,079

CURRENT FILING DATE: 2002-06-21

PRIOR PPLICATION NUMBER: 09/562,909

PRIOR PELING DATE: 2000-05-02

PRIOR FILING DATE: 1995-06-05

PRIOR FILING DATE: 1995-06-05

PRIOR FILING DATE: 1994-11-18

NUMBER OF SEQ ID NOS: 9

SEQTWARE: Patentin Version 3.1

SEQ ID NO 9
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APPLICATION DATA:

APPLICATION NUMBER: US/09/929,752

FILING DATE: 14-Aug-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/555,905

FILING DATE: <UNKnown>
APPLICATION NUMBER: UP 7-215798

FILING DATE: 24-Aug-1995

APPLICATION NUMBER: JP 6-326611

FILING DATE: 28-DEC-1994

APPLICATION NUMBER: JP 7-007177

FILING DATE: 20-JAN-1995

APPLICATION NUMBER: JP 7-007177

FILING DATE: 20-JAN-1995

APPLICATION NUMBER: JP 7-007177

FILING DATE: 10-JAN-1995

APPLICATION NUMBER: JP 7-007177

FILING DATE: 10-JAN-1995

APPLICATION NUMBER: JP 7-007177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 16-MAR-1995
APPLICATION NUMBER: JP 7-224544
FILING DATE: 10-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAVIG G.
REGISTRATION NUMBER: 27,026
Sequence 9, Application US/10176079 Publication No. US20020192760A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 GIDWFLFWVF 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 GIDFIIFWIF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZĮP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-176-079-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-929-752-2
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ZUL109
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUBBER: US/09/929,752
FILING DATE: L4-Mg-2001
PRIOR APPLICATION NUBBER: US 7-215798
FILING DATE: 24-Mg-1995
APPLICATION NUBBER: JP 7-215798
FILING DATE: 20-JAN-1995
APPLICATION NUBBER: JP 7-057186
FILING DATE: 10-MAR-1995
APPLICATION NUBBER: JP 7-224544
APPLICATION NUBBER: JP 7-224544
APPLICATION NUBBER: JP 7-224544
APPLICATION NUBBER: JP 7-057186
FILING DATE: 10-MAR-1995
APPLICATION NUBBER: JP 7-224544
APPLICATION NUB
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CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/09929752
Publication No. US20030113909A1
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
Fujii, Ryo
Kawamata, Yuji
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
PRODUCTION AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.9%; Score 45; DB 9; Length 343; 60.0%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
REFERENCE/DOCKET NUMBER: 1550/45836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: peptide

FRACMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-929-752-2
                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-440
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TYPE: 343 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                  STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity bureast Local Similarity
6; Conservative
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256 GIDWFLFWVF 265
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STATE: MA
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US-09-929-752-9
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 9, 2003, 15:05:28 ; Search time 7.22124 Seconds (without alignments) 213.004 Million cell updates/sec Run on:

US-09-854-133-587 98 1 FQANCGIDFIIFWIFW 16 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	ALGA protein - wes	Process		G protein-compled	conserved hypothet	Fe-S oxidoreductas	probable membrane-	NADH2 dehvdrogenas			rc	2	Id heavy chain V r	probable membrane	hypothetical prote				Iq heavy chain V r	Iq heavy chain V r	Ig heavy chain V r	Iq heavy chain V r	ATPase subunit 6 -	entical prote	malic acid transpo	hypothetical prote	С	hypothetical profe	
SUMMARIES		861985	J01724	D95366	A35639	D69890	B96994	AH0415	B81252	A71937	A64647	B89823	YUMU	A30560	S64252	AB2320	T05554	C69516	S41689				2	1071	10	B64395	T25580	S25942	T19814	E71163
	DB	2	Н	~	~	1	~	7	n	7	Т	7	Н	7	7	7	7	Н	7	7	7	7	7	7	7	7				
	Length	544	262	491	343	179	391	284	332	475	519	545	804	121	147	194	256	329	483	123	127	130	134	194	Н	342	345	495	585	123
dР	Query	51.0	49.0	48.0		44.9	٠	٠	43.9	٠	•	•		42.9	•	•	42.9		42.9	•	٠	41.8	٠	٠	٠	•	•	41.8	٠	41.3
	Score	50	48	47	45	44	44	43	43	43	43	43	43	42	42	42	42	42	42	41	41	41	41	41	41	41		41	4	40.5
	Result No.	П	7	e	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24			27	28	29

|| : || | ||| 514 NCAVGFICFSIFW 526 4 NCGIDFIIFWIFW 16

Ωp οy

hypothetical prote	NADH2 dehydrogenas	hypothetical prote			hypothetical prote	Ig heavy chain V r	hypothetical prote	ABC-type sugar tra	probable membrane	hypothetical 37.9K	hypothetical profe	hypothetical profe	probable membrane	hypothetical prote	
AD2556	859109	T47828	E84723	B82692	T03811	836257	T28778	G96981	AC0489	S47742	B91179	C86025	AE0986	C64216	G86220
~	~	7	7	7	7	~	7	7	~	~	~	7	~	7	7
	9	8	7	0	_	•									
318	99	83	103	7	9	119	221	289	309	337	337	337	342	375	378
				40.8 7											
41.3	41.3	41.3	41.3		40.8	40.8	40.8	40.8	40.8	40.8	40.8	40.8	40.8	40.8	40.8

# ALIGNMENTS

RESULT 1 S61985 ALG6 protein - yeast (Saccharomyces cerevisiae) N;Alternate names: protein O2513; protein UNA544; protein YOR002w	
<pre>C;Species: Saccharomyces cerevisiae C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000 C;Accession: S61985; S66867; S72134 R:Sterky, F.: Uhlen, M</pre>	
A;Molecule type: DNA A;Residues: 1-544 <ste> A;Cross_references: EMBL:U43491; NID:g1150992; PIDN:AAC49481.1; PID:g1150997</ste>	
<pre>K; Pettersson, B.; Sterky, F.; Uhlen, M. submitted to the Protein Sequence Database, July 1996 A; Reference number: \$66682</pre>	
A; Molecule type: DNA A; Residues: 1-544 <pet></pet>	
A)CLOSSTRETERENCES: EMBL:Z/4910; NID:g1420089; PIDN:CAA99190.1; PID:g1420090; MIPS A)Experimental source: strain S288C R;Sterky, F; Holmberg, A.; Pettersson, B.; Uhlen, M. Yeast 12, 1091-1095, 1996	(IPS:
A; Title: The sequence of a 30 kb fragment on the left arm of chromosome XV from Sac A; Reference number: \$72130; MUID: 97051599; PMID: 8896276 A; Accession: \$72134	n Sac
A;Status: nucleic acid sequence not shown; translation not shown A;Aolequle type: DNA A:Desiduce: 1.544 / cmus	
L:U43491; NID:g1150992; PIDN:AAC49481.1; PID:g1150997 sequence was submitted to the EMBL Data Library, December	er 19
A;Gene: SGD:ALG6 A;Cross-references: SGD:S0005528; MIPS:YOR002w A;Map position: 15R	
C; Keywords: transmembrane protein F;40-56/Domain: transmembrane #status predicted <tml> F;145-16/I/Domain: transmembrane #status predicted <tm2> F;221-237/Domain: transmembrane #status predicted <tm3> F;222-278/Domain: transmembrane #status predicted <tm4> F;326-278/Domain: transmembrane #status predicted <tm4> F;36-352/Domain: transmembrane #status predicted <tm5> F;36-352/Domain: transmembrane #status predicted <tm5> F;509-525/Domain: transmembrane #status predicted <tm6></tm6></tm5></tm5></tm4></tm4></tm3></tm2></tml>	
Query Match 51.0%; Score 50; DB 2; Length 544; Best Local Similarity 61.5%; Pred. No. 3.8; Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;	

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C; Species: Rattus norvegicus (Norway rat)
C; Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 16-Jul-1999
C; Accession: A35639
R; Ross, P.C.; Figler, R.A.; Corjay, M.H.; Barber, C.M.; Adam, N.; Harcus, D.R.; Ly Proc. Natl. Acad. Sci. U.S.A. 87, 3052-3056, 1990
Proc. Natl. Acad. Sci. U.S.A. 87, 3052-3056, 1990
A; Fitle: RTA, a candidate G protein-coupled receptor: cloning, sequencing, and tis A; Reference number: A35639; MUID:90222168; PMID:2109324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M35297; NID:g206809; PIDN:AAA42087.1; PID:g206810; GB:M3209
C;Superfamily: mas transforming protein
C;Keywords: G protein-coupled receptor; glycoprotein; membrane protein
F;4/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cipecies: Bacillus subtilis
Cipecies: Bacillus subtilis
Cipecies: Bacillus subtilis
Cipecies: Bacillus subtilis
Cipecies: D6989
Cipecies: Bacillus subtilis
Cipate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
Cipacession: D69800
R;Kunst, F:; Ogasawara, N:; Moszer, I:; Albertini, A.M.; Alloni, G:; Azevedo, V.;
R;Kunst, F:; Ogasawara, D:; Entian, C.V.; Caldwell, B: Capuano, V:; Carter, N.M.
C:; Bron, S:; Brouillet, S:; Bruschi, C.V.; Caldwell, B:; Capuano, V:; Carter, N.M.
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.;
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.;
A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Lapidus, A.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Port A; Authors: Schleich, S.; Schroeter, B.; Rose, M.; Sadale, Y.; Sato, T.; Sato, T.; Minters, M.; Tamakoth, A.; Tanaka, T.; Terpstra, P.; Toshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subt A; Reference number: A69580; MUID:98044033; PMID:9384377
A; Reference number: Asserting and sequence of the Gram-positive bacterium bacillus subt A; Reference number: A69580; MUID:98044033; PMID:9384377
A; Actaus: Positian and power and sequence of the Gram-positive bacterium bacillus subt A; Accession: D6890
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A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 15;
3; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical protein yndM - Bacillus subtilis
3;
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4; Mismatches
    Mismatches
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C;Superfamily: hypothetical protein ycbP
                                                                                                                                                                                                                                                                                                                                                        G protein-coupled receptor RTA - rat
        4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.9%;
60.0%;
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94 ADFGLSFVILWVF 106
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Best Local Similarity 60.0
Matches 6; Conservative
        Conservative
                                                                             5 CGIDFIIFWIFW 16
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A; Residues: 1-343 <ROS>
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        Matches
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                                                                                      δλ
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                                                                                                                                                                                                                                                                                                               C; Accession: JQ1724
R; Horsburgh, B.C.; Brierley, I.; Brown, T.D.K.
J. Gen. virol. 73, 2849-2862; 1992
A; Title: Analysis of a 9.6 kb sequence from the 3' end of canine coronavirus genomic RNP
A; Reference number: PQ0481; MUID:93057357; PMID:1431811
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A Status: preliminary
A Mocession: D95366
A Status: preliminary
A Mocession: DA
A Pesidues: 1-491 - KURN-
A Cross references: GB:AE006469; PIDN:AAK65494.1; PID:g14523966; GSPDB:GN00165
A Cross references: GB:AE006469; PIDN:AAK65494.1; PID:g14523966; GSPDB:GN00165
A Experimental source: strain 1021, megaplasmid pSymA Abola, P.; Ampe, F.; Barloy-Hubler, P.; Stalibert, F.; Finan, T.M.; Long, S.R.; Pulner, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Schence 293, 668-672, 2001
A Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, Hebault, P.; Vandenbol, M. Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.A.; A; Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A Reference number: A96039; MUID:21368234; PMID:11474104
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                                                                                                              J01724

El membrane glycoprotein precursor - canine coronavirus (strain Insavc-1)
N'Alternate names: matrix glycoprotein
C;Species: canine coronavirus
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Molecule type: genomic RNA
A.Molecule type: genomic RNA
A.Residues: 1-262 <HOR>
A.Cross-references: DDBJ:D13096; NID:g406193; PIDN:BAA02413.1; PID:g406200
A.Cross-references: DDBJ:D13096; NID:g406193; PIDN:BAA02413.1; PID:g406200
C.Genetics:
A.Gene: M
G.Gone: M
C.Superfamily: coronavirus El membrane glycoprotein
C.Superfamily: coronavirus El membrane glycoprotein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-72/Product: El membrane glycoprotein #status predicted <MAT>
F:56-72/Product: El membrane #status predicted <TMAD>
F:56-72/Domain: transmembrane #status predicted <TMAD>
F:115-134/Domain: transmembrane #status predicted <TMAD>
F:115-134/Domain: transmembrane #status predicted <TMAD>
F:115-134/Domain: transmembrane #status predicted <TMAD
F:115-134/Domain: transmembrane #status predicted <FROM (Covalent) #status predicted
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C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Keywords: oxidoreductase
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Pred. No.
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Matches 6; Conservative
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Best Local Similarity
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                                                                                  RESULT 2
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A;Molecule type: DNA
A;Residues: 1-332 <PAR>
A;Cross-references: GB:AL139079; GB:AL111168; NID:g6968971; PIDN:CAB73560.1; PID:g6
A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Variety: strain J99
C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 20-Aug-1999
C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 20-Aug-1999
C; Accession: A71937
S; Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, S; Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, S; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G Nature 397, 176-180, 1999
A; Title: Genomic sequence comparison of two unrelated isolates of the human gastric A; Reference number: A71800; MuID:99120557; PMID:9923682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GB:AE001439; NID:g4154929; PIDN:AAD05979.1; PID:g4
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A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Frase A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MUID:97394467; PMID:9252185
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C;Superfamily: arginine permease
C;Keywords: amino acid transport; glycoprotein; transmembrane protein
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C;Species: Helicobacter pylori
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A64647
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Pred. No. 43;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                     Length 332;
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C;Superfamily: NADH dehydrogenase (ubiquinone) chain 1
C;Keywords: membrane-associated complex; NAD; oxidoreductase
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C,Species: Helicobacter pylori
                                                                                                                                                                                                                                                                  43.9%; Score 43; DB 2; 75.0%; Pred. No. 30; tive 0; Mismatches
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Pred. No. 40;
5; Mismatches
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A; Residues: 1-475 <ARN>
A; Cross-references: GB: AE001474; G
A; Experimental source: strain J99
C; Genetics:
A; Gene: jhp0406
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Best Local Similarity 36.4%;
Matches 4; Conservative
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Matches 4; Conservative
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nes 6; Conserv
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                                                                                                                        A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: B96994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Yersinia postis
C; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C; Accession: AH0415
R; Prenthill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, A; Title: Genome sequence of Yersinia postis, the causative agent of plague.
A; Reference number: AB0001; MUID:21470413; PMID:11586360
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C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
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A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: B81252
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A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GB: AL590842; PIDN: CAC92652.1; PID: 915981349; GSPDB: GN00175
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K; Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, Nature 403, 665-668, 2000
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Pred. No. 24;
4; Mismatches
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Best Local Similarity
''^a 6; Conserv?
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Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-391 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-284 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: CAC0765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: ampE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics
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hypothetical protein all4113 [imported] - Nostoc sp. (strain PCC 7120)
C; Species: Nostoc sp.
A; Note in Strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C; Accession: AB2320
R; Raneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irin Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Taba DNA Res. 8, 205-213, 2001
A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A; Reference number: AB1807; MUID:21595285; PMID:11759840
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-147 <FAR>
A; Cross-references: EMBL:272752; NID:g1322886; PID:g1322887; GSPDB:GN00007; MIPS:YGI
A; Experimental source: strain S288C
C; Genetics:
A; Gene MIPS:YGL230C
A; Cross-references: SGD:S0003199
                                                       A; Title: Variable region cDNA sequences and antigen binding specificity of mouse mor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Molecule type: DNA
A,Residues: 1-194 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB75812.1; PID:g17133248; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable membrane protein YGL230c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein G0946
C;Species: Saccharomyces cerevisiae
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 19-Apr-2002
C;Accession: S64252
R;Fartmann, B.; Kramer, B.; Kramer, W.
Submitted to the Protein Sequence Database, May 1996
A;Reference number: S64248
A;Accession: S64252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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C.Superfamily: Saccharomyces cerevisiae probable membrane protein YGL230c
C;Keywords: transmembrane protein
F;89-105/Domain: transmembrane #status predicted <TWM>
                                                                                                                                           A;Accession: A30560
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-121 < MAIT>
A;Cross-references: GB:MZ2955; NID:g195610; PIDN:AAA38368.1; PID:g195611
C;Superfamaily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology < IMM>
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                                                                                                            A; Reference number: A30560; MUID:89110062; PMID:2464028
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Pred. No. 18;
2; Mismatches
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Pred. No. 21;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 7 Match 42.9%;
Local Similarity 50.0%;
Local 7; Conservative
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50.0%;
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R; Matsuda, T.; Kabat, E.A.
J. Immunol. 142, 863-870, 1989
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6; Conservative
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C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 11-Jun-1999
C.Accession: S19125
R.Chopra, S.; Del-Favero, J.; Dolferus, R.; Jacobs, M.
R.Chopra, S.; Del-Favero, J.; Dolferus, R.; Jacobs, M.
A.Title: Sucrose synthase of Arabidopsis: genomic cloning and sequence characterization.
A.Reference number: S19125
A.Title: Sucrose synthase of Arabidopsis: genomic cloning and sequence characterization.
A.Reference number: S19125
A.Status: nucleic acid sequence not shown
A.Residues: DNA
A.Residues: I-804 <CHO>
A.Residues: EMBL:X60987; NID:g16525; PIDN:CAA43303.1; PID:g16526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99
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                                                                                                                                                                                                                                                       Species: Staphylococous aurens (Silani N313)
Ciperies: Staphylococous aurens (Silani N313)
Ciperies: Staphylococous aurens (Cipate 10-May-2001 #text_change 22-oct-2001
Cipate 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-oct-2001
Cipate 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-oct-2001
Cipate 10-May-2001 #sequencing 1: Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oma, A.; Mizuttani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, Lancet 357, 1225-1240, 2001
A.; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A.; Reference number: A89758; MUID:21311952; PMID:11418146
A.; Accession: B89823
A.; Residues: 1-545 <KUR>
A.; Reperimental source: strain N315
C.; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain V region (16.4.12E) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 23-Jul-1999
C;Accession: A30560
                                                                                                                                                                                                                                 hypothetical protein araB [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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2; Mismatches
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62.5%; Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43;
Pred. No.
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50.0%;
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                        GIDFIIFWIFW 16
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C,Superfamily: ribulokinase
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Best Local S:
Matches 5
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Search completed: July 9, 2003, 15:09:49 Job time: 12.2212 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July Run on:

9, 2003, 15:05:28; Search time 1.9823 Seconds (without alignments) 334.773 Million cell updates/sec

1 FQANCGIDFIIFWIFW 16 US-09-854-133-587 98 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

. 112892 seqs, 41476328 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Maximum Match 100% Post-processing: Minimum Match 0%

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to tie score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ (			SUMMAKIES		
Result No.	Score	Query Match	Length	DB	ID	Description	
-	50	51.0	544	Н	ALG6_YEAST	Q12001 saccharomyc	, 0
~	48		262	7	VME1_CVCAI	P36299 canine ente	ø
m	45		343	Н	RTA_RAT	P23749 rattus norv	>
4	45	45.9	406	Н	G64B_DROME		
2	43		545	7	ARAB_STAAM	Q99w57 staphylococ	Ö
9	43		804	Н	SUS2_ARATH		Ø
7	42		147	Н	YGY0_YEAST		υ
æ	42	42.9		П	YL31_ARCFU	028149 archaeoglob	Q
5	42	42.9		7	FUT7_MOUSE	Q11131 mus musculu	ŋ
2	41	41.8		П	Y762_METJA	Q58172 methanococc	Ö
-	41	41.8		~	NU4M_MARPO	P26848 marchantia	
2	40.5	41.3		Н	NU5M_CHOCR	chondrus	cr
F 3	40	40.8		Н	YHJD_ECOLI		æ
4	40	. 40.8		Н	Y147_MYCGE	P47393 mycoplasma	
15	40	40.8		-	DCE1_RAT		>
9	40	40.8		Н	DCE1_FELCA	P14748 felis silve	a
7	40	40.8		Н	DCE1_HUMAN	homo	<u>_</u>
æ	40	40.8		Н	DCE1_PIG	s sns	
o,	39.5	40.3		Н	ELBA_ECOLI	esch	ಹ
õ	39	39.8		Н	VGL1_CVPR8		Ø
Ξ.	39	39.8		Н	VME1_CVPFS		ผ
2	39	39.8		Н	VME1_CVPPU	,	ಥ
33	39	39.8		7	VME1_CVPRM	-	ιΩ
<b>4</b>	39	39.8		7	VME1_FIPV		υ
22	39	39.8		П	RCEL_CHLAU	P11695 chloroflexu	n
92	39	39.8		7	MRAY_LACLA		(O
7	39	39.8		1	YA85_MYCPN	P75608 mycoplasma	
8	39	39.8		-	NADE_TREPA	083759 treponema	a
6	38	38.8		Н	HV36_MOUSE	P01806 mus musculu	Þ
0	38	38.8		Н	HV42_MOUSE	P01812 mus musculu	J
ᅼ	38	38.8		Н	HV39_MOUSE	P01809 mus musculu	Ħ
2	38	38.8	119	Н	HV37_MOUSE	P01807 mus musculu	Þ
ñ	38	38.8	119	<b>~</b>	HV38_MOUSE	P01808 mus musculu	z,

P01810 mus musculu	pos 1	Q9pht8 campylobact		Q57916 methanococc	_	_		Q99yk2 streptococc	P75585 mycoplasma		P75166 mycoplasma
HV40_MOUSE	CD63_BOVIN	TATC_CAMJE	AQP6_HUMAN	NADC_METJA	YKG8_CAEEL	MC5R_MOUSE	MC5R_RAT	MRAY_STRPY	Y147_MYCPN	Y432_MYCGE	Y432_MYCPN
1	ч	_	-	Н	Н	-	Н	Н	Н	-	Н
119	236	245	282	283	317	325	325	336	377	398	404
38.8	38.8	38.8	38.8	38.8	38.8	38.8	38.8	38.8	38.8	38.8	38.8
38	38	38	38	38	38	38	38	38	38	38	38
4	2	ڡؚ	1.7	38	6	o	Ţ.	42	m	4	2

## ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase (BC 2.4.1.-) (Dolichyl-P-Glc:Man9GlcNAc2-PP-dolichyl glucosyltransferase).
                                                                                                                                                                                                                          Sterky F., Holmberg A., Pettersson B., Uhlen M.;
"The sequence of a 30 kb fragment on the left arm of chromosome XV from Saccharomyces cerevisiae reveals 15 open reading frames, five of which correspond to previously identified genes.";
                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE ALGE/ALG8 GLUCOSYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- PATHWAY: Glycosylation.
                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGD; S0005528; ALG6.
Interpro; IPR004856; Alg6_Alg8.
Pfam: PF03155; Alg6_Alg8; 1.
Transferase; Glycosyltransferase; Transmembrane;
             544 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
              PRT;
                                                                                                                                                                                                                 MEDLINE=97051599; PubMed=8896276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U43491; AAC49481.1; -. EMBL; Z74910; CAA99190.1; -.
                                                                                                              ALG6 OR YOR002W OR UNA544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reticulum (Potential)
             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56
125
166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Endoplasmic reticulum.
                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                        NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105
146
           ALG6_YEAST
Q12001;
01-NOV-1997 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
ALG6_YEAST
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CGIDFIIFWIFW 16

οy

81 CGIKMLIMWLLW 92

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                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93057357; PubMed=1431811;
Horsburgh B.C., Brierley I., Brown T.D.K.;
"Analysis of a 9.6 kb sequence from the 3' end of canine coronavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                           Canine enteric coronavirus (strain Insavc-1) (CCV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - FUNCTION: TARGETS THE SITE OF VIRUS MORPHOGENESIS AND MAY BE IMPLICATED IN VIRAL PATHOGENESIS.
- SUBCELLULAR LOCATION: LARGELY EMBEDDED IN THE LIPID BILAYER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL).
O-LINKED (POTENTIAL).
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SIMILARITY: BELONGS TO THE CORONAVIRUS M PROTEIN FAMILY.
                                                                                                                                             Score 50; DB 1; Length 544; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 48; DB 1; Length 262;
                                                                                                                                                                                                                                                                                                             01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last Sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
El glycoprotein precursor (Matrix glycoprotein) (Membrane
                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                   64BFA11A1F6D02B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LINKED (GLUNAC. . .) (P
35C6D45DC6A474F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matrix protein; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O-LINKED (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E1 GLYCOPROTEIN. POTENTIAL.
                                                                                                                                                                                                                                                                                       262 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1.4;
                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                   POTENTIAL. POTENTIAL.
                                                                                        POTENTIAL.
                                        POTENTIAL.
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                           POTENTIAL
                                                                               POTENTIAL
               POTENTIAL
                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genomic RNA.";
J. Gen. Virol. 73:2849-2862(1992),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; JQ1724; JQ1724.
InterPro; IPR002574; Corona_M.
                                                                                                                   62782 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29508 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D13096; BAA02413.1; -.
                                                                                                                                            51.0%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.0%;
                                                                                                                                                                                                                       514 NCAVGFICFSIFW 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01635; Corona M; 1
                                                                                                                                                                                               4 NCGIDFIIFWIFW 16
                                                                                                                                                        Best_Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262
72
101
134
32
33
44
55
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56
85
115
32
33
44
55
                                                                                                                   544 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=36391;
                                                                                                                                                                                                                                                                                                                                                                     glycoprotein).
                                                                                                                                                                                                                                                                                      VME1_CVCAI
P36299;
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TRANSMEM
TRANSMEM
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CARBOHYD
CARBOHYD
                                                              TRANSMEM
TRANSMEM
                                                                                        TRANSMEM
TRANSMEM
                                      FRANSMEM
                                                   TRANSMEM
                                                                                                                   SEQUENCE
                                                                                                                                             Query Match
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TRANSMEM
            FRANSMEM
                         FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                            RESULT 2
VME1_CVCAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
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FTTFTFF
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                                                                                                                                                                                                                                                                                                                                                                       -i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- TISSUE SPECIFICITY: GUT, VAS DEFERENS, UTERUS, AND AORTA BUT ONLY BARELY DETECTABLE IN LIVER, KIDNEY, LUNG, AND SALIVARY GLAND. IN THE BRAIN, RIA IS MARKEDLY ABUNDANT IN THE CERBELLUM.
-i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                        STRAIN Sprague - Dawley; TISSUE-Aorta; MEDLINE-9022168; PubMed-2109324; Ross P.C., Figler R.A., Corjay M.H., Barber C.M., Adam N., Ross P.C., Egler R.A., Corjay M.H., Barber C.M., Adam N., "RTA, a candidate G protein-coupled receptor: cloning, sequencing, and tissue distribution."; Proc. Natl. Acad. Sci. U.S.A. 87:3052-3056(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
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Pred. No. 5.2;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A35639; A35639.
InterPro; IPR002276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm.l. 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYTOPLELLILLA.
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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E4630007770941F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                              01-NOV-1991 (Rel. 20, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
Probable G protein-coupled receptor RTA.
                                343 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 (POTENTIAL)
                                  PRT;
                                                               01-NOV-1991 (Rel. 20, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38364 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M35297; AAA42087.1; -. EMBL; M35298; AAA42088.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.9%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOST SIMILAR TO MAS.
                                                                                                                                               Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        343 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
TRANSMEM
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Matches
               RTA_RAT
RESULT
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RA Amanatidas P.C., Scherer S.E., Lip P.W., Broakins R.A., Galle R.F.,
Ramanatidas P.C., Scherer S.E., Lip P.W., Broakins R.A., Galle R.F.,
Ramanatidas P.C., Scherer S.E., Lip P.W., Hookins R.A., Galle R.F.,
Sutton G.G., Wortman J.R., Yandell W.D., Zhang Q., Chen L.X.,
Ramanatidas P.C., Baxter E.G., Helt G., Champen M., Pichifer P. Man K.H., Doyle C., Baxter E.G., Helt G., Champen M., Pichifer P. Man K.H., Doyle C., Baxter E.G., Helt G., Champen M., Pichifer P.,
Ballew R.M., Basu A., Baxenalle J., Bayraktaroglu L., Basaley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bahandari D., Bolshakov S.,
Burtis K.C., Busam D.A., Bulter H., Cadieu E., Center A., Chandra I.,
Ramatak R., Doyle C., Parlace H., Cadieu E., Center A., Chandra I.,
Ramatak R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Ramatak R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Ramatak R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
Ramatak R., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Rosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
Ramatak R., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Rangellan M., Kalush F., Kazpen G.H., Ke Z., Kenison J.R., Natelson D.L.,
Randli M., Kalush F., Kazpen G.H., Ke Z., Kenison J.R., Matteil B., Kodire C.D., Howland T.J., Warny D.M., Nacleon D.R., Mutholy L., Murny D.M., Nacleon D.R., Nacleon M.P., Morbherson D.,
Randali M., Kalush R.A., Mortosh R.A., Musskern D.R., Peese M.G.,
Randali M., Nelson R.A., Mornes M., Skupski M.P., Smith T.,
Spirakas R., Tector C., Turner R., Venter E., Shen H.,
Spirakas R., Tector C., Turner R., Venter E., Shen H.,
Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q., Zheng I.,
Williams S.M., Wester B.W., Rubin G.M., Wenter J.C.,
Scheeler F., Spradling A.W., Zhou X., Zhu X., Zhu X., Saith H.O.,
Schence 287:2185-2195720001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dunipace L., Meister S., McNealy C., Amrein H.; "Spatially restricted expression of candidate taste receptors in the Drosophila gustatory system."; Curr. Biol. 11:822-835(2001).
                                                                                                                                                                                                                                                                                                 Eukaryota: Metazoa; Arthoroda; Madibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                       P83294; OSV2J7;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Robertson H.;
Unpublished observations (NOV-2001).
                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly)
                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Berkeley;
MEDLINE=20196006; Pubmed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21407712; PubMed=11516643;
                                                                                                                                                                                                                                            Putative gustatory receptor 64b. GR64B OR CG14986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 287:2185-2195(2000).
                                                                                                                                          STANDARD;
                   |||::||:|
256 GIDWFLFWVF 265
6 GIDFIIFWIF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONCEPTUAL TRANSLATION
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DENTIFICATION
                                                                                                                                          G64B_DROME
                                                                                               RESULT 4
G64B_DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=21311952; PubMed=11418146;

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,

Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,

Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,

"Whole genome sequencing of meticillin-resistant Staphylococcus
aureus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                         {\tt CAUTION:\ Ref.1} sequence differs from that shown due to erroneous gene model prediction.
              -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                        EMBL; AE003480; AAF47821.1; ALT_SEQ.
Flybase; Fegn0045478; Gr64b.
Hypothetical protein; Receptor; G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.9%; Score 45; DB 1; Length 406;
                                                                                                                                                                                                                                                                                                      1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus (strain Mu50 / ATCC 700699), and Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=158878, 158879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F6A37DD9E1E58B88 CRC64;
Probable role in the gustatory response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
1-ribulokinase (EC 2.7.1.16)
ARAB OR SAV0552 OR SA0510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          545 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5-JUN-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47488 MW;
                                            RECEPTORS. SUBFAMILY II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lancet 357:1225-1240(2001)
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291 NIGVDFLVMLAFW 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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79
100
130
1151
1151
1183
204
204
2286
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370
391
406
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les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        406 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARAB_STAAM
Q99W57;
                                                                                                                                                                                                                                                                                                                        DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                     DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                           TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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Matches
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Length 804;

91989 MW; 3E727D3CDFF9A4B9 CRC64;

804 AA;

SEQUENCE

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01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation u
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MEDLINE-9211921; PubMed=1531031;
Chopra S., Del-Favero J., Dolferus R., Jacobs M.;
Chopra S., Del-Favero J., Dolferus R., Jacobs M.;
"Sucrose synthase of Arabidopsis: genomic cloning and sequence characterization."; 11-134(1992).
-! FUNCTION: SUCROSE-CLEAVING ENZYME THAT PROVIDES UDP-GLUCOSE AND FRUCTOSE FOR VARIOUS METABOLIC PATHWAYS.
-! CATALYTIC ACTIVITY: UDP-91ucose + D-fructose = UDP + sucrose.
-! INDUCTION: BY ANAEROBIC STRESS.
-! SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1. PLANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
   CATALYTIC ACTIVITY: ATP + L-ribulose = ADP + L-ribulose 5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR000577; FGGY_kin.
Pfam; PF00370; FGGY_1.
Pfam; PF00370; FGGY_1.
Pfam; PF02782; FGGY_2.
Transferase; Kinase; Arabinose catabolism; Complete proteome.
SEQUENCE 545 AA; 60965 MW; E3917036237CEA4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.9%; Score 43; DB 1; Length 545; 50.0%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                              SIMILARITY: BELONGS TO THE RIBULOKINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transferase; Glycosyltransferase; Multigene family.
                                                                 L-arabinose catabolism; second step
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               804 AA.
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InterPro; IPR000368; Sucrose_synth.
Pfam; PF00534; Glycos_transf_1; 1.
Pfam; PF00862; Sucrose_synth; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AP003359; BAB56714.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X60987; CAA43303.1; -. PIR; S19125; YUMU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                BAB41741.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 RSNCGLGFKAFW 206
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les 6; Conserv
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NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AP003130;
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Q00917;
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                                                    Gaps
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STRAIN-VC-16 / DSM 4304 / ATCC 49558;
MEDLINE-98049343; PubMed-9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                    ;
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0
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01-0cT-1996 (Rel. 34, Last sequence update)
01-0cT-1996 (Rel. 34, Last annotation update)
Hypothetical 17.3 kDa protein in SEC15-SAP4 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.9%; Score 42; DB 1; Length 147; 50.0%; Pred. No. 7.2; 4; Indels iive 2; Mismatches 4; Indels
                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Fartmann B., Kramer B., Kramer W.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 AA; 17262 MW; F8F040AlD618CD96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
                                                                                                                                                                                                                                                                                                                                                         Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                 Score 43; DB 1;
Pred. No. 23;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                        147 AA
                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
                   43.9%; Score 43;
62.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Transmembrane.
TRANSMEM 85 105 POTENTI
                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaeoglobaceae; Archaeoglobus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; 272752; CAA96948.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein AF2131
Query Match
Best Local Similarity 62...
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 42.9
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 CAIQFLFFIIYW 107
                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 CGIDFIIFWIFW 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGD; S0003199; YGL230C.
                                                                                                                      19 FLSFWVFW 26
                                                                                     9 FILFWIFW 16
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-0CT-2001
16-0CT-2001
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                                                                                                                                                                                                     YGYO_YEAST
P53074;
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028149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                         YGYO_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YL31_ARCFU
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Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-NIH Swiss,
MEDLINE-9621526; PubMed-8626519;
Smith P.L., Gersten K.M., Petryniak B., Kelly R.J., Rogers C.,
Natswa Y., Alford J.A. III, Scheidegger E.P., Natswa S., Lowe J.B.;
"Expression of the alpha (1.3) fucosyltransferase Fuc-TVI in lymphoid aggregate high endothelial venules correlates with expression of L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        selectin ligands.";
J. Blol. Chem. 271:8250-8259(1996).
-!- FUNCTION: MAY CATALYSE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN
THE EXPRESSION OF SIALYL LEWIS X ANTIGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: GDP-L-fucose + alpha-2,3-Neu-N-acetyl-1,4-beta-0-galactosyl-N-acetyl-D-glucosaminyl-R = GDP + alpha-2,3-Neu-N-acetyl-1,4-beta-D-galactosyl-(alpha-1,3-L-fucosyl)-N-acetyl-D-glucosaminyl-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                            The complete genome sequence of the hyperthermophilic, sulphate-
                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Alpha-(1,3)-fucosyltransferase (EC 2.4.1..) (Galactoside 3-L-fucosyltransferase) (Fucosyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42; DB 1; Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C07CAFD427DC26F7 CRC64;
                                                                                                                                                reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               389 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                            EMBL; AE000957; AAB89128.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37066 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304 ILFWLFW 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231
263
306
329 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                             Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LUMENAL, CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

MTPCPPACLSTPGTHRLLPFDWKAPSWESRKEATCNSSS

POGPWAEPTVO -> MNCI (IN ISOFORM 2).

118FC6B2378B99C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96337999; PubMed=868089;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.L.,
Scott J.L., Geoghagen N.S.M., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                     -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG AND BONE MARROW AND TO A MUCH LESSER EXTENT IN SPLEEN, SALIVARY GLAND AND SKELETAL
PATHWAY: Glycosylation.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
FORM IN TRANS CISTERNAE OF GOLGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00852; Glyco_transf_10; 1.
Transferase; Glycosyltransferase; Transmembrane; Glycoprotein; Signal-anchor; Golgi stack; Alternative splicing.

DOMAIN 1 55 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Euryarchaeota; Methanococci; Methanococcales;
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Pred. No. 17;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               342 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Methanocaldococcaceae; Methanocaldococcus.
NCBI_TaxID=2190;
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STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44494 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.9%;
                                                                                                                                                                                                                                                                                                                                         EMBL; U45980; AAC52484.1; -.
                                                                                                                                                                                                                                                                                                                                                              U45980; AAC52485.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein MJ0762.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.58;
                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:107692; Fut7.
InterPro; IPR001503; GT_10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methanococcus jannaschii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 GIDFIIFWIFW 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              389 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997
01-NOV-1997
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Y762_METJA
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Marchantiophyta;
Marchantiopsida; Marchantiidae; Marchantiales; Marchantiineae;
Marchantiaceae; Marchantia.
 -1- SIMILARITY: STRONG, TO M. JANNASCHII MJ0576 AND TO S. POMBE MALATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fukuzawa H., Ohyama K.;
"Cotranscriptional expression of mitochondrial genes for subunits of MADH dehydrogenase, nad4, nad4, nad2, in Marchantia polymorpha.";
MOI Gen. Genet. 237:343.350(1993).
-1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                                                               Transmembrane; Transport; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=93247547; PubMed=8483448;
Nozato N., Oda K., Yamato K., Ohta E., Takemura M., Akashi K.,
Fukuzawa H., Ohyama K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 1; Length 342; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  08EFEC3E2C4955D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1992 (Rel. 23, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
NADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    495 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
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                                                                                                                                                                                               InterPro; IPR004695; C4dic_mal_transp. Pfam; PF03595; C4dic_mal_tran; 1. TIGREAMS; TIGR00816; tdt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marchantia polymorpha (Liverwort)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 GIDFILIKNNLFLGKIFWVF 112
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                                                                                                                                                                                                                                                                                                                                                                                                                    39534 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.88;
45.08;
                                                                                                                                                                   EMBL; U67521; AAB98753.1; -.
TIGR; MJ0762; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ochondrial genome.";
Mol. Biol. 223:1-7(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                            99
                                                                                                                                                                                                                                                                                                         128
162
195
2227
262
296
                                                                                                                                                                                                                                               Hypothetical protein;
               PERMEASE (MAE1).
                                                                                                                                                                                                                                                                                                                                                                                                                 342 AA;
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nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3197;
                                                                                                                                                                                                                                                                                                                                                      207
242
276
304
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              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Rhodophyta; Florideophyceae; Gigartinales; Gigartinaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leblanc C., Boyen C., Richard O., Bonnard G., Grienenberger J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete sequence of the mitochondrial DNA of the rhodophyte Chondrus crispus (Gigartinales). Gene content and genome corpanization."

J. MOL. Biol. 250:484-495(1995).

-I- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                 Score 41; DB 1; Length 495;
Pred. No. 31;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                       Intertry. Pro0361; oxidored q1; 1. Pfan: PF00131; NUOXDRDTASE4. Oxidoreductase; NAD; Ubiquinone; Mitochondrion. SROUENCE 495 AA; 56311 MW; 0F75894D6CAAAED4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 666 AA; 75628 MW; 37E86F2C24B9D360 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
NADH-ubiquinone oxidoreductase chain 5 (EC 1.6.5.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 48;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.3%; Score 40.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, 247547; CAA87625.1; -.
Interpro; IPR003916; NADHub_oxred5.
Interpro; IPR001750; Oxidored_q1.
Interpro; IPR001516; Oxidored_q1.
                                                                                                                                            PIR; S25942; S25942.
InterPro; IPR003918; NADHub_oxred4.
InterPro; IPR001750; Oxidored_q1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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MEDLINE=95341681; PubMed=7616569;
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Pfam; PF00662; oxidored_q1_N; 1.
PRINTS; PR01434; NADHDHGNASE5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ND5 OR NAD5.
Chondrus crispus (Carragheen).
                                                                                                                                                                                                                                                                                         41.88;
                                                                                                                           EMBL; M68929; AAC09398.1; -.
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135 CSLDLLIFYVFF 146
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 41.7
Matches 5; Conservative
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Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kloared B.;
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NU5M_CHOCR
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Query Match
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MEDLINE=94316500; PubMed=8041620;
Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
Analysis of the Escherichia coli genome. V. DNA sequence of the
region from 76.0 to 81.5 minutes.";
Nucleic Acids Res. 22:2576-2586(1994).
-: SIMILARITY: STRONG, TO E.CHRYSANTHEMI HYPOTHETICAL PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=ATCC 33530 / G-37;
MEDLINE=96026346; PubMed=7569993;
Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB 1; Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; Complete proteome. SEQUENCE 337 AA; 37911 MW; C41B2A224902E311 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P4/32),
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                       01-001-1994 (Rel. 30, Created)
01-001-1994 (Rel. 30, Last sequence update)
16-001-2001 (Rel. 40, Last annotation update)
Hypothetical protein yhjD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 31;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE000428; AAC76547.1; -.
EcoGene; EG12248; yhjb.
InterPro; IPR005274; Cons_hypoth766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR004664; RNase_BN.
Pfam; PF03631; Ribonuclease_BN; 1.
TIGRFAMS; TIGR00766; TIGR00766; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDGK 5'REGION (AC P45417).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U00039; AAB18498.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.88;
                          | : || |:|||:|
176 FGLSLGI-FLIFWVF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.48;
1 FOANCGIDFIIFWIF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein MG147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycoplasma genitalium.
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244 LFFWIFW 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                              Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y147_MYCGE
P47393;
                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia
                                                                                                                                                                            YHJD_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                       P37642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y147_MYCGE
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                                                                                                                              RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L., Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M., Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Julien J.F., Samama P., Mallet J.; "Rat brain glutamic acid decarboxylase sequence deduced from a cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning, characterization, and autoimmune recognition of rat islet glutamic acid decarboxylase in insulin-dependent diabetes mellitus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                        "The minimal gene complement of Mycoplasma genitalium.";
Science 270:397-403(1995).
-:- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-FBF-1996 (Rel. 33, Last annotation update)
61-tamate decarboxylase, 67 kDa isoform (EC 4.1.1.15) (GAD-67)
(67 kDa glutamic acid decarboxylase).
GADI OR GAD67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Michelsen B.K., Petersen J.S., Boel E., Moldrup A., Dyrberg T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDINE=91014554; PubMed=2170798; Wyborski R.J., Bond R.W., Gottlieb D.I.; "Characterization of a cDNA coding for rat glutamic acid
                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A14AF07D574E8046 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brain Res. Mol. Brain Res. 8:193-198(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL. POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92020930; PubMed=1924335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neurochem. 54:703-705(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43188 MW;
                                                                                                                                                                                                                                                                                                                                                              EMBL; U39695; AAC71365.1; -.
TIGR; MG147; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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181
223
254
309
358
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239 DFLVLWIFY 247
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                                                                                                                                                                                                                                                                                                                                                                                                               protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      375 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DCE1_RAT
P18088;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ü
Proc. Natl. Acad. Sci. U.S.A. 88:8754-8758(1991).
-! FUNCTION: CATALXZES THE PRODUCTION OF GABA.
-! CATALXZES THE PRODUCTION OF GABA.
-! CATALXZEC ACTIVITY: L-glutamate = 4-aminobutanoate + CO(2).
-! COPACTOR: PYRIDOXAL PHOSPHATE.
-! SUMILY: HOMODIMER.
-! SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
                                                                                                                                                                                                                                                                                                                                                                                                                           PYRIDOXAL PHOSPHATE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40.8%; Score 40; DB 1; Length 593;
42.9%; Pred. No. 52;
Live 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       L -> V (IN REF. 2).
F -> S (IN REF. 2).
AG -> EA (IN REF. 2).
T -> I (IN REF. 2).
T -> I (IN REF. 2).
FD -> LE (IN REF. 2).
L -> R (IN REF. 2).
L -> R (IN REF. 2).
W, EF83239C30301F69 CRC64;
                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00282; pyridoxal_dec; 1.
PROSITE; PS00392; DDC_GAA_HDC_YDC; 1.
Neurotransmitter biosynthesis; Lyase; Decarboxylase;
Pyridoxal phosphate; Multigene family.
                                                                                                                                                                                                                                              EMBL; M34445; AAC42037.1; -.
EMBL; X57572; CAA40800.1; -.
EMBL; X57573; CAA40801.1; -.
EMBL; M76177; AAA41184.1; -.
PIR; A41367; A41367.
InterPro; IPR002129; Pyridoxal_dec.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66640 MW;
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Best Local Similarity 42.50
Laca 6; Conservative
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103
284
288
345
347
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352
380
593 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
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   δ
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Search completed: July 9, 2003, 15:08:58 Job time : 11.9823 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

July 9, 2003, 15:05:28; Search time 7.22124 Seconds

(without alignments)

456.536 Million cell updates/sec

Title:

US-09-854-133-587

Perfect score:

1 FQANCGIDFIFFWIFW 16

Scoring table:

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched:

671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum Match 0%

Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries
```

## 1: Sparchea:* 2: sp_bacteria:* 3: sp_larchea:* 4: sp_luman:* 5: sp_luman:* 6: sp_luman=1:* 7: sp_lum:* 8: sp_lanc:* 10: sp_lanc:* 11: sp_rodent:* 12: sp_lunciassified:* 13: sp_lanc:* 14: sp_lanciassified:* 15: sp_larcheap:* 16: sp_larcheap:* 17: sp_larcheap:* 17: sp_larcheap:* 17: sp_larcheap:*

SPTREMBL_21:*

Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q9p9f4 methanosarc	Q8tqn5 methanosarc	Q9tdu3 echinococcu	Q9ev68 rhizobium m	Q92yn6 rhizobium m	Q958u2 echinococcu	Q8t411 brugia mala	Q8vev1 mus musculu	Q953m3 echinococcu	Q9rph1 escherichia	Q9rm48 escherichia	Q8vqr2 escherichia	Q8vnr6 escherichia	Q968z8 plasmodium	Q91zb6 mus musculu	096am1 homo sapien
SUMMARIES	ID	Q9P9F4	O8TQN5	Q9TDU3	O9EV68	092YN6	Q958U2	Q8T4L1	Q8VEV1	Q953M3	Q9RPH1	Q9RM48	Q8VQR2	Q8VNR6	0968z8	Q912B6	096AM1
	Н	1	17	æ	7	16	œ	2	11	8	7	7	7	7	5	11	4
;	Match Length DB	495	495	275	491	491	535	192	310	530	3223	3223	3223	3223	269	319	343
* Query	Match	50.0	50.0	48.0	48.0	48.0	48.0	46.9	46.9	46.9	46.9	46.9	46.9	46.9	45.9	45.9	45.9
	Score	49	49	47	47	47	47	46	, 46	46	46	46	46	46	45	45	45
Result	No.	Н	7	m	4	2	9	7	ω	6	10	11	12	13	14	15	16

Q8vcj6 mus musculu Q9na34 caenorhabdi Q02708 podospora a 031816 bacillus su Q97101 clostridium	2007	homo homo homo	_ 8 € √	09hjk7 thermoplasm 0979n1 thermoplasm 025661 helicobacte 09b8v3 schlattosoma	ຸຂວິດ	Q36097 theileria p O57661 xenopus lae Q9fmn5 arabidopsis Q9fis1 venerupis p
					•	į
Q8VCJ6 Q9NA34 Q02708 Q31816	Q9U8R4 Q95XS9 Q9V3S5	0960C5 090HQ2 090HQ3 09BRV3	Q95KW8 Q8ZBI8 Q9PMA3 Q9ZM17	Q9HJK7 Q979N1 Q25661 Q9B8V3	Q8YPS8 Q8YPS8 Q9SB30 O76204 O93875	Q36097 O57661 Q9FMN5 Q9G1S1
H 99	່ນນທຸ		16 16 16	17 17 16 8	10 10 3	8 10 8 8
343 856 149 391	531 899 1440	157 179 221 221	221 284 332 475	503 516 519 530	805 194 256 351 386	483 622 671 103
4 4 4 4 4 4 4 4 4 4 4 4 4 4 9 9 9 9 9 9					2 4 4 4 4 2 2 2 3 4 2 9 9 9 9 9	
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		4 4 4 4. 2 6 6 6 6	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4444	4 4 4 4 2 4 4 4 4	4 4 4 4 2 2 2 L
118 119 20 21	2222	0 5 5 5 6 5 6 5 6 5 6 5 6 5 6 5 6 5 6 5	30 31 32	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	3 / 3 / 4 / 4 /	4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5

## ALIGNMENTS

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Q9EV68;
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Q9EV68
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ID Q9
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                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRIN-CZA / ATCC 35395 / DSM 2834;

MEDLINE-21929760; PubMed-11932238;

MEDLINE-21929760; PubMed-11932238;

A dlagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

A Allen N., Maylor J., Stanger-Thomann N., DeArellano K., Johnson R.,

Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

A Limmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

A Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

Leigh J.A., Li W., Liu J., Mukhpadhyay B., Reeve J.N., Smith K.,

Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

R Feiry J.G., Jarrell R.F., Jing H., Macario A.J.L., Paulsen I.,

Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

RA Metcalf W.W., Birren B.;

"The genome of Methanosarcina acetivorans reveals extensive metabolic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE=21036605; PubMed=11163447;

Makao M., Sako Y., Yokoyama N., Fukunaga M., Ito A.;

Mitochondrial genetic code in cestodes.";

Mitochondrial genetic code in cestodes.";

Mol. Biochem. Parasitol. 111:415-424(2000).

-1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY

CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.0%; Score 49; DB 17; Length 495;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Cytochrome c oxidase polypeptide I (EC 1.9.3.1) (Fragment).
     Indels
                                                                                                                                                                                                  Methanosarcina acetivorans.
Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
Cyclophyllidea; Taeniidae; Echinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            495 AA; 54138 MW; 278918B16BA7BAE6 CRC64;
                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
  0
                                                                                                                 495 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 7.9;
  4; Mismatches
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                                                                                                                                                                          F(420)H(2) dehydrogenase, subunit FpoM.
                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         and physiological diversity.",
Genome Res. 12:532-542(2002).
EMBL; AE010819; AAM04919.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.08;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 60.0
                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Echinococcus granulosus.
                                                  128 LDFVVFYIFW 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 LDFVVFYIFW 137
                         7 IDFILEWIEW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 IDFIIFWIFW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome
                                                                                                                                                                                                                                          NCBI_TaxID=2214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6210;
                                                                                                                                                                                          FPOM OR MA1505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                            Q8TQN5;
                                                                                                               Q8TQN5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09TDU3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9TDU3
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                       RESULT 2
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                                                                                                    O8TON5
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3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HENE A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).

CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICYTOCHROME
                                                                                                                                                        -!- COFACTOR: HEMES A, A3, AND COPPER B (BY SIMILARITY).
-!- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY EMBL.); BAB033471;
-- INREPRO: IPRO00883; COXI.
-- PRO0115; COXI; 1.
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Bacteria; Proteobacteria; alpha subdivision; Rhizoblaceae group;
Rhizobiaceae; Sinorhizobium.
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                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR01165; CYCOXIDASEI.
PROSITE; PS00077; COX1; UNKNOWN_1.
COPPER; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47; DB 8; Length 275;
Pred. No. 9.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48.0%; Score 47; DB 2; Length 491; 41.7%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30298 MW; 20B1917902CB529D CRC64;
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SEQUENCE 491 AA; 52714 MW; A2C62574220C4EEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Putative NADH-ubiquinone oxidoreductase subunit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                         Respiratory chain; Transmembrane.
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PRINTS; PR01437; NUOXDRDTASE4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.0%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 CALDLFLFYVFW 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 CGIDFIIFWIFW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275 AA;
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SEQUENCE
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491 AA.

PRT;

PRELIMINARY;

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InterPro; IPR000883; COX1.
                                                                                                                                                                                                 Query Match
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Q8T4L1
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Le T.H., Blair D., Dai N.T.H., Pearson M., McManus D.P.;
"Echinococcus mitochondrial genome.";
"Echinococcus mitochondrial genome.";
submitted (AuG-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBNNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE
CATALYTIC SUBUNIT OF THE ENXYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER FORMED BY HEME A3
AND GOPPER B (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICYTOCHROME
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-!- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
EMBL; AF297617; AAK51685.1; -.
                                                                                                                                                                                                                                                                                                                                                            Daraline_21396509; PubMed=11481432;

Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,

Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,

Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,

Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,

Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,

Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;

"Nucleotide sequence and predicted functions of the entire

Sinorhizobium mellioti pSymA megaplasmid.";

Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).

EMBL; AE007270; AAK65494.1; -.

InterProc. Proc. Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
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COFACTOR: HEBES A, A3, AND COPPER B (BY SIMILARITY).
PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
                                                                                                                                                                                                                   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
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                                                 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
NuoM2 NaDH-ubiquinone/plastoquinone (Complex I) oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.0%; Score 47; DB 16; Length 491; 41.7%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
Cyclophyllidea; Taeniidae; Echinococcus.
NCBL_TaxID=6210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oxidoreductase; Plasmid; Complete proteome.
SEQUENCE 491 AA; 52828 MW; F197C587058FDZFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Cytochrome c oxidase polypeptide I (EC 1.9.3.1).
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                                                                                                                                           NUOMZ OR RAÓ836 OR SMA1536.
Rhizobium meliloti (Sinorhizobium meliloti)
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                         01-DEC-2001 (TrEMBLrel. 19, Created)
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                                                                                                                                                                                               pSymA (megaplasmid 1)
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CALDLFLFYVFW 138
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nes 5; Conserv
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                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                       NCBI_TaxID=382;
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                                                                                                                                                                                                                                                                                                                                                  STRAIN=1021
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                                                                                                                                                                                                 Plasmid
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Brugia.
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0
                PRINTS; PRO1165; CYCOXIDASEI.
PROSITE; PS00077; COX1; UNKNOWN_1.
COpper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
                                                                                                                                         Length 535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE FROM N.A.

Wu Y., Bianco A.E.;
"Thioredoxin of human filarial parasite Brugia malayı.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX080907; AAL91107.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22071 MW; 617B22FA86BCEA01 CRC64;
                                                                                                  60100 MW; 49944A4882F4FCED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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Last annotation update)
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InterPro; IPR000276; GPCR_Rhodpsn.
PERMIP; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhang X., Firestein S.J.;
"The olfactory receptor gene superfamily of the
Nat. Neurosci. 0:0-0(2002).
                                                                                                                                         DB 8;
18;
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                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                           Score 47;
                                                                                                                                                                Pred. No
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                                                                             Respiratory chain; Transmembrane. SEQUENCE 535 AA; 60100 MW; 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Olfactory receptor MOR261-11
                                                                                                                                         48.0%;
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                                                                                                                                                            50.08;
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145 AYCGLNEIIYWYFY 158
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                                                                                                                                                                                                                                             138 FSSSCGVDFLMF 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                          Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                       1 FQANCGIDFIIF 12
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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Best Local Similarity
7; Conserve
Pfam; PF00115; COX1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bruqia malayi.
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-1-FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDOCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE CATALYZIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).

-1-CATALYZIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE HEWE-COPPER RESPIRATORY OXIDASE FAMILY EMBL; AF346403; AAK82350.1; -. InterPro; IPR000883; COXI.
                                                                                                              Gaps
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-!- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR01165; CYCOXIDASEI.
PROSITE; PS00077; COX1; UNKNOWN_1.
COPPER; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
Respiratory chain; Transmembrane.
                                                                        Score 46; DB 11; Length 310;
Pred. No. 15;
                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Cytochrome c oxidase polypeptide I (EC 1.9.3.1) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.9%; Score 46; DB 8; Length 530; 50.0%; Pred. No. 25; Live 4; Mismatches 2; Indels
                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
Cyclophyllidea; Taeniidae; Echinococcus.
                                    310 AA; 34917 MW; 452A1D723081781D CRC64;
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SEQUENCE 530 AA; 59632 MW; 2E5FCA534DFD1771 CRC64;
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Last annotation update)
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                                                                                                         3; Mismatches
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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                                                                    Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative
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17 QLSAGIEMFLFWIF 30
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Query Match
Best Local Similarity 50.00,
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                   Receptor.
                                      SEQUENCE
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Q953M3
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RA SEQUENCE.

RY MICHOLIS L., Grant T.H., Robins-Browne R.M.;

RA Nicholls L., Grant T.H., Robins-Browne R.M.;

RI Tadhesion of a novel genetic locus that is required for in vitro andesion of a clinical isolate of enterohaemorraghic Escherichia coli RT to epithelial cells.",

RL Mol. Microbiol. 35:275-288(2000).

RE EMBL; AF159462; AAD49229.2.

DR EMBL; AF159462; AAD49229.2.

InterPro; IPR001917; NHtransf.2.

InterPro; IPR001917; NHtransf.2.

DR PROSITE; PS00639; AA_TRANSFER_CLASS_2; UNKNOWN_1.

PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.

SQ SEQUENCE 3223 AA; 365949 MW; CAFD59F69242D07A CRC64;
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MEDINE 20187489;
MEDINE 20187489;
MISTANE 20187489;
Malstrom C., James S.P., Donnenberg M.S.;
Malstrom C., James S.P., Donnenberg M.S.;
A large toxin from pathogenic Escherichia coli strains that inhibits lymphocyte activation.*;
Infect. Immun. 68:2184-2155(2000).
EMBL; AJ133705; CAB55629:1;
InterPro; IPR001917; MHransf_2.
InterPro; IPR001917; MHransf_2.
InterPro; IPR00199; AHProt_acsite.
PROSITE; PS00639; THIOL_PROFEASE HIS; UNKNOWN_1.
SEQUENCE 3223 AA; 365963 MW; 03E45ECDED7938C1 CRC64;
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                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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Escherichia.
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                                                                                                                                                                                                                                                                                                                                           46.9%; Score 46; DB 2; Length 3223;
43.8%; Pred. No. 1.4e+02;
ive 4; Mismatches 5; Indels
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43.8%; Pred. No. 1.4e+02;
Live 4; Mismatches 5; Indels
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last anno
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SHEC factor for adherence.
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Best Local Similarity 63.0.
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Best Local Similarity 43.84
Dest Local Similarity 7; Conservative
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                                                                                                         SEQUENCE FROM N.A.
            EFA1.
Escherichia coli
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                                                                          NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=562;
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Q8VQR2;
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Receptor.
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"Genetic organisation and sequence of the LEE II locus in Shiga toxin-
"Genetic organisation and sequence of the LEE II locus in Shiga toxin-
"Genetic organisation and sequence of the LEE II locus in Shiga toxin-
"Brocharing Exploration or the EMBL/GenBank/DDBJ databases.

EMBL; AJ277443; CAC81883.1; -.
InterPro; IPR001019; NHtransf_2.
InterPro; IPR001019; SHprot_acsis_2.
InterPro; IPR001059; AA_TRANSFER CLASS_2; UNKNOWN_1.

PROSITE; PS00599; AA_TRANSFER CLASS_2: UNKNOWN_1.

SEQUENCE 3223 AA, 365666 MW; 28EBB4374FABBEC7 CRC64;
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                                                       Escherichia coli.
Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia,
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                                                                                                                                Trunchek M., Strugnell R.A., Robins-Browne R.M.;
"Characterization of the LEE pathogenicity islands of rabbit enteropathogenic Escherichia coli.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR453441; AA457552.1;
InterPro; IPR001917; NHtransf_2.
InterPro; IPR001997; AA TRANSTER_CASS_2; UNKNOWN_1.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
SEQUENCE 3223 AA, 365790 MW; E97D10B98FADE658 CRC64;
                                                                                                                                                                                                                                                              Length 3223;
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                                                                                                                                                                                                                                                 46.9%; Score 46; DB 2; Length 322
43.8%; Pred. No. 1.4e+02;
Live 4; Mismatches 5; Indels
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                         01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Created)
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Best Local Similarity 43.8%;
                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=413/89-1;
                                                                                         NCBI_TaxID=562;
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Q96828
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Gaps
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STRAIN-NIGERLAN I/CDC;
MEDLINE-21192570; PubMed=11295191;
MEDLINE-21192570; PubMed=11295191;
Tachinbana M., Tsuboi T., Templeton T.J., Kaneko O., Torii M.;
Presence of three distinct ookinete surface protein genes, Pos25, Pos28-1, and Pos28-2, in Plasmodium ovale.";
Mol. Biochem. Parasitol. 113:341-344(2001).
EMBL; AB051633; BAB43950.1; -.
InterPro; IPR000561; EGF-1ike.
SMART; SM00181; EGF; 3.
PROSITE; PS01186; EGF-2: UNKNOWN_1.
SEQUENCE 269 AA; 29928 MW; 7A949BB42F036EEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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0
                                                                                         Plasmodium ovale (malaria parasite P. ovale).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dong X., Han S.-K., Zylka M.J., Simon M.I., Anderson D.J.;
"A Diverse Family of GPCRS Expressed in Specific Subsets of
Nociective Somatosensory Neurons.";
Cell 106:619-632[2001].
EMBL, AX042211; AAK91802.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
PROSITE; PS00021; 7tm_1; 1.
PROSITE; PS00021; G_PROTEIN_RECEP_FI_1; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45; DB 5; Length 269;
Pred. No. 19;
4; Mismatches 3; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Ookinete surface protein Pos28-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) G protein-coupled receptor (Fragment).
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01-DEC-2001 (TrEMBLrel. 19, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last anno
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MEDLINE=21435808; Pubmed=11551509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.9%;
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Best Local Similarity 46.20,
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92 FKCNCTRNYIVFW 104
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232 GIDWFLFWVF 241
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